n.a. database search, using Smith-Waterman algorithm n.a. MPsrch_nn MasPar time 1905.03 Seconds 1347.129 Million cell updates/sec Thu Jun 26 04:11:00 1997; Run on:

not generated Tabular output

(1-2308) from US08436265.seq >US-08-436-265-9 Description:

2308 Perfect Score: Sequence:

1 GGCGAGGCGAGGTTTGCTGG......TGTTAAAACCTATAGTGTTT 2308 CCGCTCCGCTCCAAAACGACC......ACAATTTTGGATATCACAAA

TABLE default Gap 6 Sccring table:

Query 0 Dbase 0; STD Nmatch. 333249 segs, 555961234 bases x 2 Searched:

Minimum Match 0% :- processing:

Listing first 45 summaries

embî-newll

300

1:BCT 2:FUN 3:GEN 4:HUX : N.742 6:HUM3 7:INV1 8:INV2 9:INV3 10:INV4 11:INV5 12:INV6 13:INV7 14:ORG 15:MAM 16:VRT 17:PLN 18:PRO1 19:PRO2 20:ROD 21:SYN 22:UNC

23:VIR1 24:VIR2 genbank97

Patrabase:

27:BCT3 ..: hCT4 29:BCT5 30:BCT6 31:BCT7 34:GEN1 35:GEN2 36:HTG 37:INV1 38:INV2 25:BCT1 26:BCT2 32:BCT8 33:BCT9

60:PEN4 61:PLN5 62:PLN6 63:PLN7 64:PLN8 65:PEN9 66:PEN10 67:PRI1 68:PRI2 69:PRI3 70:PRI4 71:PRI5 72:PRI6 73:PRI7 74:PRI8 75:PRI9 76:PRII0 77:PRII1 78:PRI12 79:PRII3 50:PRII4 81:ROD1 82:ROD2 83:ROD3 84:ROD4 85:ROD5 86:ROD6 39:INV3 40:INV4 41:INV5 42:INV6 43:INV7 44:INV8 45:INV9 46:MAM1 47:MAM2 48:MAM3 49:VRT1 50:VRT2 51:VRT3 52:PAT1 53:PAT2 54:PAT3 55:PAT4 56:PHG 57:PLN1 58:PLN2 59:PLN3

87:ROD7 88:RODE 89:STR 90:SYN 91:UNA 92:VRL1 93:VRL2 94:VRL2 95:VRL4 96:VRL5 57:VRL6 98:VRL7 99:VRL8 100:VRL9

101:BCT 102:GEN 103:INV1 104:INV2 105:MAM 106:VRT 107:PHG 108:PLN 109:PRI1 110:PRI2 111:ROD 112:SYN genbank-newll

Database:

113:UNA 114:VRL u-emb148 97

Database:

115:part1 116:part2

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Mean 12.312; Variance 5.693; scale 2.085

Stics:

SUMMARIES

%

| Pred. No. | 0.00e+00 |
|--------------------------|-----------------------|-----------------------|-----------------------|-----------------------|-----------------------|-----------------------|-----------------------|-----------------------|-----------------------|
| Description | Human activin recepto | Mouse mRNA for TGF-be | Mustela sp. TGF-b typ | Mouse mRNA for TGF-be | Mouse mRNA for TGF-be | Sequence 4 from paten | Sequence 4 from paten | Rat transforming grow | Chicken RPK-2 mRNA fo |
| ID | 111 | MUSTGFB1R | MSU37065 | MMTGFBTI | MUSTGFBIR | 123851 | 125010 | RATSETHKIR | CHKRPK2 |
| DB | 75 | 98 | 47 | 20 | 86 | 55 | 25 | 87 | 49 |
| Query Match Length DB | 2308 75 | 2860 86 | 1381 | 1659 | 1659 | 1506 | 1506 | 1545 | 2186 |
| Query Match | 100.0 | 54.3 | 52.9 | 49.8 | 49.8 | 47.7 | 47.7 | 47.7 | 36.1 |
| Score | 2308 | 1253 | 1221 | 1150 | 1150 | 1102 | 1102 | 1102 | 833 |
| Result No. | 1 | 7 | м | 4 | Ŋ | 9 | 7 | ω | Q |

| TOCUS | HUMALKSA | 2308 bp | mRNA | Ē. | PRI | 24-JAN-1994 | 34 |
|------------|---|------------|------------|----------|----------|-------------|-----|
| DEFINITION | DEFINITION Human activin receptor-like kinase (ALK-5) mRNA, complete cds. | receptor- | like kinas | e (ALK-5 | mRNA, | complete co | ls. |
| ACCESSION | L11695 | | | | | | |
| NID | g431034 | | | | | | |
| KEYWORDS | activin; activin receptor-like kinase; serine/threonine kinase; | vin recept | or-like ki | nase; se | rine/thr | conine kina | se; |

transforming growth factor-beta; transmembrane protein. Homo sapiens cDNA to mRNA. Homo sapiens ORGANISM SOURCE

Franzen, P., ten Dijke, P., Ichijo, H., Yamashita, H., Schulz, P., Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; 1 (bases 1 to 2308) AUTHORS REFERENCE

Cloning of a TGF beta type I receptor that forms a heteromeric complex with the TGF beta type II receptor Cell 75 (4), 681-692 (19.3) 94061986 Heldin, C.H. and Miyazono, K. TITLE

COURNAL MEDILINE

· 0 Gaps 0; Length 2308; 0; Indels Score 2308; DB 75; Pred. No. 0.00e+00; 0; Mismatches 100.0%; Best Local Similarity 100.0%; Matches 2308; Conservative Query Match

A mouse TGF-beta type I receptor that requires type II receptor for Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae; 04-OCT-1994 TGF-beta type I receptor; serine/threonine kinase receptor; Eukaryotae; mitochondriai eukaryotes; Metazoa; Chordata; Biochem. Biophys. Res. Commun. 198 (3), 1063-1069 (1994) 94161715 MUSTGFBIR 2860 bp mRWA ROD 04-0 Mouse mRWA for TGF-beta vy. 3 I receptor, complete cds. Suzuki, A., Shioda, N., Maeda, T., Tada, M. and Ueno, N. transforming growth factor-beta type I receptor. Mus musculus brain CDNZ · ··NA. (bases 1 to 2860) ligand binding Murinae; Mus. Mus musculus 9483375 D25540 ~ DEFINITION ORGANISM ACCESSION AUTHORS JOURNAL MEDLINE REFERENCE KEYWORDS TITLE RESULT LOCUS

11; Gaps 0; Mismatches 170; Indels 19; Length 2860; Score 1253; DB 86; Pred. No. 0.00e+00; Query Match
Best Local Similarity 89.0%;
Matches 1537; Conservative

31-OCT-1995 1381 bp mRNA rurur .-- TGF-b type I receptor mRNA, partial cds. Mustela sp. U37065 MSU37065 g1045609 DEFINITION ACCESSION m RESULT LOCUS NID

Eukaryotaė, mitochondrial eukaryotes, Metazoa, Chordata, Vertebrata, Eutheria, Carnivora, Fissipedia, Mustelidae, Mustela. (bases 1 to 1381) Mustela sp. mink. ORGANISM KEYWORDS SOURCE REFERENCE AUTHORS

Weis-Garcia,F. and Massague,J. Complementation between kinase-defective and activation-defective TGF-b receptors reveals a novel form of receptor cooperativity Direct Submission Submitted (26-SEP-1995) Frances Weis-Garcia, Cell Biology EMBO J. (1995) In press (bases 1 to 1381) Weis-Garcia, F. REFERENCE AUTHORS JOURNAL JOURNAL TITLE TITLE RESULT

standard; RNA; ROD; 1659 BP LT 4 MMTGFBTI D28526; g467521

AND

RESULT

ALIGNMENTS

ggatcactgcaataaaatagaactcccaactacaggaccttttcagaaaagcagtcagc AGAAATGAGAAAAGTTGTTTGTGAACAGAAGTTAAGGCCAAATATCCCAAACAGATGGCA 553 733 351 433 411 493 531 613 673 651 711 793 771 1033 1011 1093 1071 1153 1131 1213 1191 1273 1333 1393 375 471 591 853 831 913 891 973 951 1251 1311 유 셤 용 a g g ò ò ò ò ð à ò g δ 원 ð 吕 δ g ò 엄 ò 임 ò ద 유 a a ద ò ò ò ò à 5. œ 110 230 318 GGCGCCGCCGCCGCCCTCCCCGGCCCCACCCTTACAGTGTTTCTGCCACCTCTG 198 Gaps Gaps and tacaaaaggacaattttacttgtgagacagatggtctctgctttgtctcagtcaccgagac ggtggcggcggcgacgctgctcccgggggcgaaggcattacagtgtttctgccacctctg cacagacaaagttatacacaatagcatgtgtatagctgaaatcgacctaattccccgaga caggccatttgtttgttgcaccatcttcaaaaacaggggcagttacgtattgctgcaatca |Submitted (26-Jan-1994) to DDBJ by: Toshifumi Tomoda Molecular and Developmental Biology Institute of Medical Science The University TACAAAAGACAATTTTACTTGTGTGACAGATGGGCTCTGCTTTGTCTCTGTCACAGAGAC CACAGACAAAGTTATACACAACAGCATGTGTATAGCTGAAATTGACTTAATTCCTCGAGA TAGGCCGTTTGTATGTGCACCCTCTTCAAAAACTGGGTCTGTGAC-TACAACAT--ATTof counterpart for human TGF-beta type Arai K.; Tokyo, Molecular and Developmental Biology; 4-6-1 Shirokanedai, Tomoda, Institute of Medical Science, The University Minato-ku, Tokyo 108, Japan (E-mail:ynakagaw@ims.u-tokyo.ac.jp 9 Mammalia; 1506; of Tokyo 4-6-1 Shirokanedai Minato-ku Tokyo 108 Japan Phone: 05-3443-8111 Fax: 03-3443-5320. 20; Length 1659 EMBL/GenBank/DDBJ databases Donahoe, P.K., Gustafson, M., He, W. and Wang, X. Nucleic acids encoding a TGF-.beta. type 1 receptor Σ̈́ Mismatches 151; Indels Indels Length Theria; Eutheria; Rodentia; Myomorpha; Muridae; Murinae cds Muramatsu Chordata; Vertebrata; PAT Biochem. Biophys. Res. Commun. 198:1054-1062(1994) Mouse mRNA for TGF-beta type I receptor, complete Mismatches 156; 1102; DB 55; No. 0.00e+00; Query Match 49.8%; Score 1150; DB 20; Best Local Similarity 89.2%; Pred. No. 0.00e+00; Version 4) Ł) Tel:03-3443-8111(ex.660), Fax:03-3443-5320) Tomoda T., Kudoh T., Noma T., Nakazawa A., "Wolecular cloning of a mouse counterpart f 394 Patent: US 5538892-A 4 23-JUL-1996 from patent US 5538892 Created) Last updated, Location/Qualifiers /organism="unknown" р Score Pred. . 0 363 0, Submitted (26-JAN-1994) to the Eukaryota; Animalia; Metazoa; 1506 bp 47.7%; 88.9%; (bases 1 to 1506) O Conservative Conservative TGF-beta type I receptor Mus musculus (mouse) .1506 26-FEB-1994 (Rel. 38, .08-SEP-1996 (Rel. 49, Unclassified. Similarity 4 MEDLINE; 94161714. ď Sequence g1603721 Unknown. Unknown 123851 123851 1445; receptor"; Ξ. Toshifumi Query Match Local ø COUNT Tomoda 1-1659 source 1-1659 DEFINITION ORGANISM 139 199 Matches Matches 21 111 171 259 231 319 ACCESSION AUTHORS JOURNAL REFERENCE KEYWORDS FEATURES TITLE RESULT SOURCE LOCUS NID 엄 DOT DOT WWW OOS OOC OOC OOC OOC WWW WREA WRE 임 ò a ð 셤 ò à 1. 1

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RATSETHKIR 1545 bp mRNA ROD 11-DEC-1995 Rat transforming growth factor beta type I receptor mRNA, complete RESULT 8 LOCUS DEFINITION 8 1033 1011 1071 1191 613 591 673 651 733 711 793 771 853 913 973 951 1093 1153 1131 1213 1273 1251 1333 1311 1393 1371 1453 1431 1513 1491 831 891 1573 ద 8 d 8 à ŏ ò 40 δ 임 g Db g 임 원 g g g В ò 3 ò ŏ ò ò ò à à δ a à 엄 à misr1, methods Š, 1512 318 410 492 470 552 530 612 Gaps 1 (bases 1 to 1506) Donahoe, P.K., Gustafson, M. and He, W.W. DNA encoding a receptor for Mullerian inhibitory substance, agcagctaggctgacagctttgcgaattaaaaaaacattgtcacagctcagccaacagga caggccatttgtttgtgcaccatcttcaaaaacaggggcagttacgtattgctgcaatca ggatcactgcaataaaatagaactcccaactacaggaccttttcagaaaagcagtcagc gagctgtgaggccttgagagtgatggccaaaattatgagagaatgttggtatgccaatgg TAGGCCGTTTGTATGTGCACCCTCTTCAAAAACTGGGTCTGTGAC-TACAACAT--ATTtttaattttatgatatgacaacatcagggtctggatcaggtttaccactgcttgttcaaag and corresponding vectors, cells, probes, and recombinant Patent: US 5547854-A 4 20-AUG-1986; 9 Length 1506 Indels PAT Score 1102; DB 55; Pred. No. 0.00e+00; Mismatches 156; د: 394 DNA US 5547854. Location/Qualifiers 1..1506 /organism="unknown" ۵ı 0; 363 patent Query Match
Best Local Similarity 88.9%;
Matches 1294; Conservative 1506 1588 1506 from pa aggcatcaaaatgtaa |||||||||||||| AGGCATCAAAATGTAA Unclassified. 4 Ø Sequence I25010 91604880 428 Unknown Unknown 125010 RESULT 7 LCCUS DEFINITION ACCESSION NID KEYWORDS SOURCE source BASE COUNT ORIGIN ORGANISM ENCE HORS 111 199 259 1371 1513 1573 171 231 319 291 375 351 433 411 493 471 553 1453 1431 1491 531 JOURNAL FEATURES ·유 g g δ Do. δ rg R ò 원 a ò D à 임 ò 엄 δ Dp ò a ò à A Art. **建、等**源· , O. <u>.</u> · 多数数

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SFKRADIYAMGLVFWEIARRCSIGGIHEDYQLPYYDLVPSDPSVEEMRKVVCEQKLRP
NIPNRWQSCEALRVMAKIMRECWYANGAARLTALRIKKTLSQLSQQEGIKM"
                                                                                                                                                            Developmental expression of four novel serine/threonine kinase receptors homologous to the activin/transforming growth factor-beta
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RGKWRGEEVAVKIFSSREERSWFREAEIYQTVMLRHENILGFIAADNKDNGTWTQLWL
VSDYHEHGSLFDYLNRYTVTVEGMIKLALSTASGLAHLHMEIVGTQGKPAIAHRDLKS
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                                                                                     Eukaryotae, mitochondrial eukaryotes, Metazoa, Chordata,
Vertebrata, Eutheria, Rodentia, Sciurognathi, Myomorpha,
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                                                        Rattus norvegicus (strain Sprague-Dawley) cDNA
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No. 0.00e+00;
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/clone="R4"
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                                                                                                                                                 He, W.W., Gustafson, M.L., Hirobe, S. and
                                                                                                                                                                                                                                                                                                                                                                            organism="Rattus norvegicus"
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N.A. Nucleotide sequence of a cDNA encoding the thicken receptor protein Submitted (06-APR-1993) Peter P ten Dijke, Ludwig Institute for Cancer Research, Uppsala, branch, Biomedical Center, Husargatan 3, 7; ö MasPar time 220.72 Seconds 967.382 Million cell updates/sec Nohno,T., Sumitomo,S., Ishikawa,T., Ando,C., Nishida,S., Noji,S. Activin receptor-like kinases: a novel subclass of cell-surface receptors with predicted serine/threonine kinase activity Oncogene 8 (10), 2879-2887 (1993) 93390967 1470 agcagctaggctgacagctttgcgaattaaaaaaacattgtcacagctcagccaacagga 1529 09-DEC-1993 29-SEP-1993 Gaps CHKRPK2 2186 bp mRNA VRT 09-DEC-199: Chicken RPK-2 mRNA for receptor protein kinase, complete cds. Gaps - n.a. database search, using Smith-Waterman algorithm serine/threonine kinase; transmembrane protein. Gallus gallus (library: lambda gt10) stage 24-26 (Hamburger Hamilton) cDNA to mRNA, clones S5 and S7. Gallus gallus Eukaryotae, mitochondrial eukaryotes, Metazoa, Chordata, Vertebrata, Eutheria, Primates, Catarrhini, Hominidae, Homo ALX-4 gene; cell surface receptor; serine threonine kinase. Uppsala, S-751 24, Sweden
2 (bases 1 to 2333)
ten Dijke,P., Ichijo,H., Franzen,P., Schulz,P., Saras,J.,
Toyoshima,H., Heldin,C.H. and Miyazono,K. Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; 0; Mismatches 240; Indels 18; .; 0 Vertebrata; Archosauria; Aves; Neognathae; Galliformes Score 832; DB 49; Length 2186; Pred. No. 0.00e+00; Length 2333; TGF-beta receptor-related, receptor protein kinase, Indels PRI 0; Mismatches 244; Score 481; DB 70; Pred. No. 0.00e+00; kinase of the TGF-beta receptor family HSALK4A 2333 bp RNA Homo sapiens ALK-4 mRNA, complete CDS. >US-08-436-265-9 (1-2308) from USO8436265.seq 2308 Phasianidae; Phasianinae; Gallus. 1 (bases 1 to 2186) 26 04:43:27 1997; DNA Seq. 3 (6), 393-396 (1993) Quary Match.

Best Local Similarity 82.1%;
Matches 1181; Conservative 20.8%; 74.8%; 1 (bases 1 to 2333) ten Dijke, P.P. 1530 aggcatcaaaatgtaa 1545 1573 AGGCATCAAAATGTAA 1588 Conservative Direct Submission not generated. Thu Jun Homo sapiens Eest Local Similarity and Saito, T. 94033626 g285699 9402188 D14460 Z22536 human. 725; n.a. Tabular output Perfect Score: Query Match Description: 13 σ DEFINITION ORGANISM DEFINITION ORGANISM TITLE HORS MPsrch_nn Matches JOURNAL MEDLINE ACCESSION AUTHORS REFERENCE AUTHORS MEDLINE ACCESSION FINCE REFERENCE JOURNAL TITLE KEYWORDS KEYWORDS TITLE RESULT Run on: SOURCE RESULT SOURCE Title: LOCUS LOCUS NID - 유 g

| Ż | .A. Sec Cor | Seguence: Comp: | | 1 GGCC CCGC | SAGG | GGCGAGGCGAGGTTTGCTGG CCGCTCCGAAACGACC | GTGTTAAAACCTATAGTGTTT .CACAATTTTGGATATCACAAA | IAGIGIIT 2308 ATCACAAA |
|----------|----------------|--|---------------------|--------------------------------------|----------------------|--|--|---------------------------------|
| й | Scoring | table: | TABLE Gap 6 | iE defaul 6 | ılt | | | |
| Ē | Nmatch | STD : | Dbase | 0; | Query | 0 \ | | |
| Š | Searched | ď.: | 121476 | 176 seqs, | | 46255616 bases | s x 2 | |
| Ä | ost-pr | Post-processing | | Minimum Mat Listing fi | Match | 0% 45 summaries | | |
| Q | Database | v | n-96 | partl 2 part8 9 part8 1:part14 | 2:pa 9:pa 1.15 | rt2 3:part3 rt9 16:part1 :part15 16:g | <pre>geneseq26 1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7 8:part8 9:part6 1C:part10 11:part11 12:part12 13:part13 14:part14 15:part15 16:part16 17:part17 18:part18 19:part19 20:part20 21:part21 22:part22 23:part23</pre> | 7:part7 3:part13 18 23 |
| ss | Statistics | ics: | Mean 9 | 9.949; | > | Variance 6.392; | 12; scale 1.557 | |
| | P) ar | Pred. No. score gre and is de | is thater trived | ne numbe than or by anal | eque | E results pr al to the so s of the tot | No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed derived by analysis of the total score distribution. | ve a printed, |
| Re | Result No. | 00 6 6 | % Query Match | % Query Match Length | EG EG | SUMMARIES | Description | Dred NO |
| • | | | 1 0 | 9000 | - | | 1 | |
| | ⊣ 7 | 1163 | 50.4 | 2308 1794 | 14 | Q67638 Q83534 | о н | 0.00e+00 0.00e+00 |
| | € 4 | 1102 | 47.7 | 1506 | 22 | T36068 049766 | | 0.00e+00 |
| | ימי | 481 | 20.8 | 2333 | 11 9 | 066637 | Human Activin recepto | 2.37e-290 |
| | 9 1 | 471 | 20.4 | 1518 | 11 % | Q49764 Q66641 | Misr2A/misr2B. Mouse Activin recepto | 1.01e-283 1.01e-283 |
| | οο σ | 467 | 20.2 | 1647 | 14 | 083533 | Sequence encoding ser | 4.50e-281 |
| | 10 | 445 | 19.3 | 1482 | 70 | T26994 | Serine threonine kina | 1.67e-266 |
| | | | | | | ALIGNMENTS | | |
| RE | S | 1 | | | | | | |
| ID P | | Q66638 sta | ndard, | standard; cDNA; | 230 | 8 вР. | | |
| E E | | -JAN-199 | 5 (£i | rst ent | :ry) | | | |
| DE | | nan Acti | vin re | ceptor- | like | Human Activin receptor-like kinase 5 (| (hALK-5) cDNA. | |
| KW | | rine thr ansformi | eonine | kinase wth fac | 153; CT | activin rece TGF: diagn | serine threonine Kinases; activin receptors; Act-R; superfamily; transforming growth factor: TGF: diagnostics: detection: therapy: | !y; |
| KW | | eumatoid | arthr | itis; g | lome | rular nephr | itis; fibrosis; ss. | 174 |
| SO | | Homo sapiens | ns. | 1 | (| , the state of the | | |
| FT | | s'UTR | | 176 | Ž | Locacion/Quailiteis 176 | | |
| FT | | H | | | | | | |
| F | | ote= "co | ntains | an in- | frar | ne stop codon | n at | |
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| PD | | -MAY - 199 | 4. | 727 | | | | |
| PR | | -NOV-199 | 3; GUL 2; GB- | 024057. | | | | |
| PR | | -MAR-199 | 3; GB- | 004677. | | | | |
| 7 Q | | 08-MAK-1993; GB-004680. 28-MAY-1993; GB-011047. | 3; GB- | 004680. 011047. | | | | |

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CCGCTCCGCTCCAAACGACC.....ACAATTTTGGATATCACAAA
New isolated TGF-beta type I receptor DNA - used to develop prods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           He WW;
                                                                                                                                                                                                                                                                                                               o,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 53; Fig 4; 59pp; English.
                                                                                                                                                                                                                                                                                                                                                            049766 standard; cDNA; 1506 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        bone morphogenesis protein; ss.
                                                                                                                                                                                                                                                            428 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   428 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          >US-08-436-265-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            47.78;
                                                                                                                                                                                                                                                                                                 Best Local Similarity 88.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity 88.9%;
                                                                                                                                                                                                                                                                                                                                                                                         20-APR-1994 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gustafson M,
                                                                                                                                                                                                                                                                                                             Matches 1294; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (GEHO ) GEN HOSPITAL CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 1294; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tabular output not generated.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-MAR-1992; US-853396.
11-MAR-1993; US-029673.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-MAR-1993; U02387.
                                                                                                                                                                                                                                                            1506 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1506 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 93-320743/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        inhibin receptors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P-PSDB; R41923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-SEP-1993.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO9319177-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Donahoe PK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                n.a.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Perfect Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N.A. Sequence:
                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seguence
                                                                                                                                                                                                                                                                                      Query Match
                                       Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                claimed
                                                                                                                                                                                                                                                                                                                                                                            049766;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Description:
                          wound
                                                                                                                                                                                                                                                                                                                                                                                                       Misr4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Comp:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MPsrch_nn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Run on:
                                                                                                                                                                                                                                                                                                                                                    RESULT
  0; Mismatches 156; Indels 27; Gaps 11;
                                                                                                                                                                                                                                                                                                                                                                                                                 inhibit the effects of BMP's such as BMP-2 and BMP-4. The truncated
                                                                                                                                                                                                                                                                                                                                                                                                                                           The truncated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mullerian inhibiting substance receptor coding sequence misr4. Mullerian inhibiting substance receptor; MISR; TGF-beta receptor;
                                                                                                                                                    Bone morphogenic protein, receptor; serine/threonine kinase, BMD; bone; cartilage; injury; treatment; inhibition; ss.
                                                                                                                                                                                                                                                                                                                                                                                                     serine/threonine kinase receptors may be used in compositions to
                                                                                                                                                                                                                                                                                                                                                                                                                          receptors pref. comprise the ligand binding domain, but not the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Such cells can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      transforming growth factor beta type I receptor; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             delivered in a medium or matrix which partially impedes their
                                                                                                                                                                                                                                                                                                                                                                                                                                                      proteins are soluble and will be excreted into supernatant by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 14; Length 1794;
                                                                                                                                                                                                                                                                                                                                                   Truncated BMP and serine/threonine kinase receptor proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mobility, thereby localising the cells to a site of bone or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     462 T;
                                                   Yamashita H;
                                                                                                                                           Sequence encoding serine/threonine kinase receptor W120.
                                                                                                                                                                                                                                                                                                                                                                                       Truncated bone morphogenic protein (BMP) receptors and
                                                                                                                                                                                                                                                                                                                                                                                                                                           serine/threonine kinase and transmembrane domains.
                                                                                                                                                                                                                                                                                                                                                              used to inhibit the effects of BMP-2 and/or BMP-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     454 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    wound healing; tumour treatment; rat inhibin; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 1163; DB 14;
Pred. No. 0.00e+00;
                                                   Miyazono K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    recombinant mammalian cells expressing them.
                                                                                                                                                                                                                                                                                                            Thies RS, Wozney JM, Yamaji N;
                                                                                                                                                                                                                             /product= Serine/threonine kinase receptor.
W09507982-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wang X;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     390 C;
                                                                                                                                                                                                                                                                                                                                                                            Claim 3; Page 64-66; 83pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   He W,
                                                  Franzen P, Heldin C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           T
T36068 standard; cDNA; 1506 BP.
                                       (LUDW-) LUDWIG INST CANCER RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     488 A;
                                                                                                      Q83534 standard; DNA; 1794 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             50.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         89.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gustafson M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-MAR-1992; US-853396.
11-MAR-1993; US-029673.
04-NOV-1993; US-149105.
(GEHO ) GEN HOSPITAL CORP.
                                                                                                                              28-SEP-1995 (first entry)
                                                                                                                                                                                                                                                                                                 GEMY ) GENETICS INST INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                           83..1594
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02-JUL-1993; GB-013763.
03-AUG-1993; GB-016099.
15-OCT-1993; GB-021344.
                                                                                                                                                                                                                                                                                     17-SEP-1993; US-123934.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-MAR-1992; 853396.
                                                                                                                                                                                                                                                                        07-SEP-1994; U10080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1794 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Donahoe PK, Gusta:
WPI; 96-353830/35.
P-PSDB; W03758.
                                                                                                                                                                                                                                                                                                             Celeste AJ, Thies WPI; 95-131350/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      UNIV DUKE.
                                                               WPI; 94-183503/22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cartilage injury
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'product= MISR4
                                                                                                                                                                                                                                                                                                                                       2-PSDB; R70241.
                                                                                                                                                                                                                                                            23-MAR-1995.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 1481;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US5538892-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-JUL-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-0CT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus sp.
                                                   Dijke P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    T36068;
                                                                                                                   083534;
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GGCGAGGCGAGGTTTGCTGG......TGTTAAAACCTATAGTGTTT 2308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1014.493 Million cell updates/sec
                                                                                                                                                             regions within the count encouring a manner of and porcine TGF-beta type II receptor and the daf-1 receptor of C-elegans. The primers (see T36072 and T36073) were used for amplifying clones present in a 14.5 day foetal rat urogenital ridge cDNA COS cell expression library. Four clones encoding portions of force and analyzed control and analyzed serine/threonine kinases)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               - n.a. database search, using Smith-Waterman algorithm
                                                                                                                                                                                                                                                                                                                                            four novel polypeptides (all putative serine/threonine kinases) were obtained and designated pGEM7-Misr1, 2, 3 and 4. The inserts from these clones were used as probes to isolate full-length cDNA sequences for each of the four TGF-beta type I receptors. Misr1 is believed to encode an isoform of the rat Mullerian Inhibiting
                                                                                                            Degenerate PCR primers were designed based on two highly conserved regions within the cDNA encoding a murine activin receptor, human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Substance (MIS) receptor, while misr2A/misr2B, misr3 and misr4 are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Thu Jun 26 04:47:38 1997; MasPar time 1458.40 Seconds
diagnosis and therapy, e.g. for treating tumours or promoting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       believed to encode monomeric isoforms of the rat inhibin receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and/or BMP receptor. The present sequence is \min sr4; isolated \widehat{D}NA able to hybridise to this sequence under stringent conditions is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             family - comprising Mullerian Inhibitory Substance Receptors and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Misrl (049763) is believed to encode an isoform of the rat
MIS receptor. Misr2A/misr2B (049764), misr3 (049765) and misr4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Q49766) are believed to encode monomeric isoforms of the rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1506;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 8; Length 1506;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        394 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches 156; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  363 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        363 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches 156;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        47.7%; Score 1102; DB 22;
88.9%; Pred. No. 0.00e+00;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MIS; Mullerian Inhibitory Substance; receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        membrane serine/threonine kinase receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                transforming growth factor; inhibin; BMP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  321 C;
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                                                                         Columns 33-36; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 inhibin receptor and/or BMP receptor
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TABLE default Gap 6 Scoring table:

Query Dbase 0; .. STD Nmatch 887282 segs, 320523884 bases x Searched:

Minimum Match 0% Post-processing:

Listing first 45

summaries

SUMMARIES Description Match Length DB EST-STS Query Score Database: No. Result

3.47e-210 4.04e-172 9.48e-135 1.45e-126 mc33h08.rl Soares mou 2.08e-116 0.00e+00 zk74e04.rl Soares pre 0.00e+00 zf53c07.rl Soares ret 3.47e-210 4.04e-172 Pred. No. 0.00e+00 using Smith-Waterman algorithm Human placenta cDNA 5 zf53c07.rl Soares ret mc85f09.rl Soares mou zc18q04.rl Soares par Muman placenta cDNA 5 zk74e04.rl Soares pre human STS WI-7314. HSA53838 HSA47142 database search, AA053838 HSC6799 AA047142 W48139 G06514 W39552 W34981 C17679 8 230 10 43 165 168 164 515 515 404 631 720 426 426 739 471 739 n. a. n.a. 720 3332 332 132 132 114 96 MPsrch nn 4500000

MasPar time 86.86 Seconds Thu Jun 26 05:12:37 1997; Run on:

854.056 Million cell updates/sec

Tabular output; not generated.

>US-08-436-265-9 (1-2308) from US08436265.seq 2308 Description:

1 GGCGAGGCGAGGTTTGCTGG......TGTTAAAACCTATAGTGTTT 2308 CCGCTCCGCTCCAAACGACC......ACAATTTTGGATATCACAAA Perfect Score: N.A. Sequence:

default TABLE Gap 6 Scoring table:

Query 0 Dbase 0; STDNmatch bases 60653 segs, 16071407 Searched:

2

Listing first 45 summaries Minimum Match 0% Post-processing:

ase:

1:51 2:52 3:53 4:54 5:55 6:56 7:PCT90 8:PCT91 9:PCT92 10:PCT93 11:PCT94 12:PCT95 13:PCT96 n-issued

scale 1.734 Variance 5.413; Mean 9.385; Statistics: No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. Pred. No.

SUMMARIES

| | | | | | | | | σ. | | |
|------------|-----------------------------|-------------|-------------|-------------|-------------|--------------|------------|------------|-------------|------------|
| | Pred. No. | 0.00e+00 | 0.00e+00 | 0.00e+00 | 0.00e+00 | 0.00e+00 | 0.00e+00 | 4.51e-299 | 8.90e-165 | 4.75e-164 |
| | | Applicatio | Applicatio | Applicatio | Applicatio | Applicatio (| Applicatio | Applicatio | Applicatio | Applicatio |
| | 6 | 6 | 4, | | | | 7 | 7, | | 2, |
| | Description | Sequence 9, | Sequence 4, | Sequence 4, | Sequence 7, | Sequence 2, | Sequence | Sequence | Sequence 3, | Sequence |
| | ID | PCT-US94-1 | US-08-149- | US-08-317- | PCT-US94-1 | US-08-149- | US-08-317- | US-08-341- | PCT-US94-1 | PCT-US95-0 |
| | DB | 11 | വ | Ŋ | 11 | വ | Ŋ | 9 | 11 | 12 |
| | Query Match Length DB ID | 1794 11 P | 1506 | 1506 | 1647 | 1506 | 1506 | 1482 | 2076 11 | 2932 |
| \ 0 | Query Match | 50.4 | 47.7 | 47.7 | 20.5 | 20.0 | 20.0 | 19.3 | 11.4 | 11.3 |
| | Score | 1163 | 1102 | 1102 | 467 | 462 | 462 | 445 | 262 | 261 |
| | Result No. | | 2 | М | 4 | ß | 9 | 7 | œ | σ |

PCT-US94-1 Sequence 1, Applicatio 2.03e-152 1813 11 ALIGNMENTS 10.6 245

10

7T 1 PCT-US94-10080-9 STANDARD; DNA; UNC; 1794 XXXXXX RESULT

BP

PC/TUS9410080 Sequence 9, Application 01-JAN-1900

Application PC/TUS9410080 GENETICS INSTITUTE, GENERAL INFORMATION: APPLICANT: Sequence 9,

RECEPTOR PROTEINS NUMBER OF SEQUENCES: TITLE OF INVENTION:

CORRESPONDENCE ADDRESS: **日間といいといい**

11; Gaps 0; Mismatches 156; Indels 27; Pred. No. 0.00e+00; Query Match 50.4%; Sest Local Similarity 89.0%; Matches 1481; Conservative

Length 1794;

Score 1163; DB 11;

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Tue Jun 24 17:58:06 1:97; MasPar time 10.36 Seconds 529.135 Million cell updates/sec Run on:

Tabular output not generated.

(1-503) from US08436265.pep >US-08-436-265-10 Perfect Score: Description:

1 MEAAVAAPRPRLLLLUVLAAA.....TALRIKKTLSQLSQQEGIKM 503 Sequence:

PAM 150 Gap 11 Scoring table:

92623 segs, 10896596 residues Searched:

0% 45 summaries Listing first Post-processing: Minimum Match

i:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13 4.part14 15.part15 16.part16 17.part17 18.part18 a-geneseq26 19:part19 Database:

scale 0.228 Variance 157.139; Mean 35.793; Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Pred. No. | 0.00e+00 | 0.00e+00 | 0.00e+00 | 0.00e+00 | 7.49e-229 | 7.49e-229 | 9.38e-229 | 1.17e-228 | 2.46e-225 | 7.30e-216 | |
|-------------------------------|-----------------------|-----------------------|----------------------|----------|-----------------------|-----------------------|----------------|-----------------------|----------------------|-----------------------|------------|
| Pre | | _ | 0. | 0. | 7.4 | 7.4 | 9 | 7 | 2.4 | 7.3 | |
| Description | Human Activin recepto | Serine/threonine kina | Mullerian inhibiting | MISR4. | Serine/threonine kina | Mouse Activin recepto | MISR2A/MISR2B. | Human Activin recepto | Mullerian inhibiting | Serine threonine kina | |
| ID | ; — | R70241 | W03758 | R41923 | R70240 | R55373 | R41921 | R55369 | W03760 | R95562 | ALIGNMENTS |
| DB | 10 | 13 | 18 | φ | 13 | 10 | ω | 10 | 18 | 17 | AL |
| % Query Match Length DB | 503 | 503 | 501 | 501 | 505 | 505 | 505 | 505 | 501 | 493 | |
| % Query Match | 99.2 | 94.7 | 93.7 | 93.7 | 68.3 | 68.3 | 68.2 | 68.2 | 67.3 | 64.7 | |
| Score | 3657 | 3493 | 3454 | 3454 | 2517 | 2517 | 2516 | 2515 | 2481 | 2384 | |
| Result No. | 7 | 7 | m | 4 | ß | 9 | 7 | œ | δ | 10 | |

503 RESULT DA CE

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20-JAN-1995 (first entry) Human Activin receptor-like kinase 5 (hALK-5). RS5370 standard; Protein; RS5370; 20-JAN-1995 (first entry)

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Best Local Similarity
                                                                                                                                                                                        503 AA;
                                                     WPI; 95-131350/17
                                                                                                                                                                               cartilage injury
                                                              N-PSDB; 083534.
   WO9507982-A
           23-MAR-1995
                                                                                                                                                                                        Sequence
                                                                                                                                                                                                          Query Match
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        transforming growth factor; IGF; diagnostics; detection; therapy; rheumatoid arthritis; glomerular nephritis; fibrosis.
   kinases; activin receptors; Act-R; superfamily;
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Serine/threonine kinase receptor W120.
Bone morphogenic protein; receptor; serine/threonine kinase;
bone; cartilage; injury; treatment; inhibition.
                                                                                                                                                                                        503
                                                                                                                                                                                                        Indels
                                                                                                                                                                                        Length
                                                                                                                                                                                                         2,
                                                                                                                                                                                        10;
                                                                                                                                                                                        Score 3657; DB 10;
Pred. No. 0.00e+00;
                                                                                                                                                                                                         1; Mismatches
                                                                       /label= activin receptor-like kinase
                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             503
                                                      signal peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R70241 standard; Protein; 503
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                                                                                                                                                                               (LUDW-) LUDWIG INST CANCER
                                                                                                                                                                                        99.2%;
                                                                                                                                                                                                99.4%;
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                                                                                                                                                                                                          Conservative
                                                                               /note= "mature protein"
                                                                                                                 17-NOV-1992; GB-024057.
7-10-1993; GB-004677.
62-MAR-1993; GB-004680.
                                                                                                                                            26-MAY-1993; GB-011047.
                                                                                                                                                     02-JUL-1993; GB-013763
                                                                                                                                                             C3-AUG-1993; GB-016099,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R70241;
28-SEP-1995 (first
                                                                                                         17-NOV-1993; G02367
                                                                                                                                                                                               t Local Similarity
ches 500; Conser
                                                      /label= putative
Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              musculus.
                                                                                                 26-MAY-1994.
                              Homo sapiens
                                                                                         WO9411502-A.
                                                                                                                                                                                        Query Match
                                              Peptide
                                                                                                                                                                                                                                                                                                                                                   181
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Claim 26; Page 67-68; 83pp; English.

Truncated bone morphogenic protein (BMP) receptors and serine/threonine kinase receptors may be used in compositions to inhibit the effects of BMP's such as BMP-2 and BMP-4. The truncated receptors pref. comprise the lighting binding domain, mut not the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SSPGLGPVELAAVIAGPVCFVCISIALMVYICHNRTVIHHRVPNEEDPSLDRPFISEGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 meaaaaaprrpqllivlvaaat----llpgakalqcfchlctkdnftcetdglcfvsvte
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                                                                                                                                                                                                                                                                                                                                            serine/threonine kinase and transsembrane domains. The trunca
proteins are soluble and will be excreted into supernatant by
recombinant mammalian cells expressing them. Such cells can b
delivered in a medium or matrix which partially impedes their
mobility, thereby localising the rells to a site of bone or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    transforming growth factor beta type I receptor; gene therapy;
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8
                                                                                                                                                              proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 503,
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Mullerian inhibiting substance receptor MISR4.
Mullerian inhibiting substance receptor; MISR; TGF-beta
                                                                                                                                                                 receptor
                                                                                                                                                                                      used to inhibit the effects of BMP-2 and/or BMP-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94.7%; Score 3493; DB 13; 95.7%; Pred. No. 0.00e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5; Mismatches
                                                                                                                                                            Truncated BMP and serine/threonine kinase
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W03758 standard; Protein;
W03758;
                                                    (GEMY ) GENETICS INST INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   485; Conservative
07-SEP-1994; U10080.
17-SEP-1993; US-123934.
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236 236 296 356 356 416 416 476 476

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Gaps

56 9

protein; receptor; serine/threonine kinase; JT 6 R55373 standard; Protein; 505 68.3%; 71.2%; Query Match 68.3%; Best Local Similarity 71.2%; (first entry) (GEMY) GENETICS INST INC 356; Conservative 356; Conservative 26-MAY-1994. 17-NOV-1993; G02367. 17-NOV-1992; GB-024057. 08-MAR-1993; GB-004677. GB-013763. 17-SEP-1993; US-123934. GB-004680 GB-011047 03-AUG-1993; GR-016099 15-OCT-1993; GB-021344 07-SEP-1994; U10080. Best Local Similarity 505 AA; cartilage injury. morphogenic bone; cartilage; N-PSDB; Q83533. Mus musculus. 08-MAR-1993; 28-MAY-1993; musculus WO9411502-A. 02-JUL-1993; 20-JAN-1995 WO9507982-A. 23-MAR-1995 Query Match Sequence R55373; Matches 73 246 Matches 184 Mus RESULT g ò g g d ò ò à 4, 414 416 57 ttdkvihnsmciaeidliprdrpfvcapssktgavt--yccnqdhcnkielpttgpfsek 114 115 gsaglgpvelaaviagpvcfvcialmlmvyichnrtvihhrvpneedpsldrpfisegtt 174 9 26 Gaps 175 lkdliydmttsgsgsglpllvgrtiartivlgesigkgrfgevwrgkwrgeevavkifss 177 LKDLIYDMTTSGSGSGLPLLVQRTIARTIVLQESIGKGRFGEVWRGKWRGEEVAVKIFSS 417 IGGIHEDYQLPYXDLVPSDPSVEEMRKVVCEQKLRPNIPNRWQSCEALRVWAKIMRECWY 1 meaasaalrrc1111ivlvaaat----11pgakalqcfchlctkdnftcetdglcfvsvte iggihedyqlpyydlvpsdpsveemrkvvceqklrpnipnrwqscealrvmakimrecwy 10; Score 3454; DB 18; Length 501; Pred. No. 0.00e+00; 9; Indels /label TATP_binding_site /note= "corresponds to conserved GXGXXGXVX(11-28)K tumour treatment; rat inhibin 5; Mismatches motif found in all serine/threonine kinases and thought to form an ATP binding site" Wang R70240; 28-SEP-1995 (first entry) Serine/threonine kinase receptor W101. Location/Qualifiers angaarltalrikktlsqlsqqegikm 3 477 ANGAARLTALRIKKTLSQLSQQEGIKM Æ Ā He R70240 standard; Protein; 505 R41923 standard; Protein; 501 93.7%; 95.3%; Donahoe PK, Gustafson M, (first entry) GEN HOSPITAL CORP 483; Conservative 210..230 11-MAR-1993; US-029673. 04-NOV-1993; US-149105. 18-MAR-1992; US-853396. 18-MAR-1992; 853396 Best Local Similarity (U.L.-) UNIV DUKE. WPI, 96-353830/35. N-PSDB; T36068. wound healing; R41923; 20-APR-1994 MISR4. Binding_site 23-JUL-1996. US5538892-A. Rattus sp. Ċ, 237 415 475 235 Matches Due Free Fr RESULT
ID R7
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DT 28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               inhibit the effects of BMP's such as BMP-2 and BMP-4. The truncated receptors pref. comprise the ligand binding domain, but not the serine/threonine kinase and transmembrane domains. The truncated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 71 pkvelvpagkpfycl-sse--dlrnthccyidfcnkidlrvpsghlkepahpsmwgpvel 127
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                                                                                                                                                                                                                                                                                                                                                                                       Claim 25, Page 63-64; 83pp; English.
Truncated bone morphogenic protein (PM-2) receptors and
serine/threonine kinase receptors R447 we used in compositions to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    transforming growth factor; TGF; diagnostics; detection; therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          serine threonine kinases; activin receptors; Act-R; superfamily;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         recombinant mammalian cells expressing them. Such cells can be delivered in a medium or matrix which partially impedes their mobility, thereby localising the cells to a site of bone or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62; Mismatches 65; Indels 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           serine/threonine kinase and transmembrane domains. The trunce proteins are soluble and will be excreted into supernatant by
                                                                                                                                                                                                                                                                                                                               proteins
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                                                                                                                                                                                                                                                                                                                               Truncated BMP and serine/threonine kinase receptor
                                                                                                                                                                                                                                                                                                                                                            used to inhibit the effects of BMP-2 and/or BMP-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 2517; DB 13;
Pred. No. 7.49e-229;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62; Mismatches 65;
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Pred. No. 7.49e-229;
injury; treatment; inhibition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mouse Activin receptor-like kinase 4 (mALK-4).
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WPI; 95-131350/17.
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244 REAEIYQTVMLRHENILGFIAADNKDNGTWTQLWLVSDYHEHGSLFDYLNRYTVTVEGMI 303
                   yglpyydlypsdpsieemrkvvcdqklrpnvpnwwqsyealrvmgkmmrecwyangaarl 485
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protein - protein database search, using Smith-Waterman algorithm Tue Jun 24 17:58:55 1997; MPsrch pp

MasPar time 18.25 Seconds 785.825 Million cell updates/sec Lar output not generated

1 MEAAVAAPRPRLLLLVLAAA......TALRIKKTLSQLSQQEGIKM 503 (1-503) from US08436265.pep 3687 >US-08-436-265-10 Perfect Score: Description: Sequence: Title:

Scoring table: FAM 150

٨

89912 seqs, 28507787 residues Searched:

4. Listing first 45 summaries Post-processing: Minimum Match 0%

Database:

1:ann1 2:ann2 3:ann3 4:ann4 5:unann1 6:unann2 7:unann3 8:unann4 9:unann5 10:unann6 11:unann7 12:unann8 13:unann9 14:unann10 15:unenc 16:unrev pir50

scale 0.425 Mean 48.912; Variance 115.163; Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Pred. No Query Result

| No. | No. Score Match Length DB 1D | Match | Length | DB | ID | Description | Pred. |
|-------------|------------------------------|--------|------------|------|-------------------------------|--|-------|
| 1 1 1 | 3687 | 100.0 | 503 | 13 | A49432 | activin receptor-lik | 0.00e |
| 7 | 3536 | 95.9 | 499 | 14 | JC2062 | transforming growth | 0.00e |
| m | 3493 | 94.7 | 503 | 14 | JC2061 | transforming growth | 0.00e |
| 4 | 3020 | 81.9 | 440 | 13 | A56693 | receptor protein kin | 0.00e |
| ß | 2522 | 68.4 | 505 | 13 | I38859 | activin receptor Act | 0.00e |
| 9 | 2522 | 68.4 | 505 | 13 | 137164 | ALK-4 - human | 0.00e |
| 7 | 2516 | 68.2 | 505 | 14 | 153417 | type I serine-threon | 0.00e |
| 80 | 2204 | 59.8 | 476 | 13 | I80182 | activin type I recep | 0.00e |
| σ | 2021 | 54.8 | 601 | 12 | A55921 | serine/threonine kin | 0.00e |
| 10 | 1893 | 51.3 | 487 | 13 | 180183 | activin type I recep | 0.00e |
| RESULT | 1 | | | | | | |
| ENTRY | | A49432 | 32 | #ty | #type complete | | |
| TITLE | | acti | activin re | cept | or-like kina | receptor-like kinase 5 precursor - human | |
| ALTERNA | ALTERNATE_NAMES | | eta tyj | oe I | TGFbeta type I receptor ALK-5 | J.K - 5 | |
| CONTAINS | က | prot | ein ki | nase | protein kinase (EC 2.7.1.37) | 37) | |

177 iydmttsgssglpllvqrtiartivlqesigkgrfgevwrgkwrgeevavkifssreer

| ORGANISM DATE | #formal_name Homo sapiens #common_name man 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change na-han-1996 |
|---|---|
| ACCESSIONS REFERENCE | 1001 11 1001 10 |
| #aucilors | Franzen, F.; ten Dijke, F.; ichijo, H.; kamasnita, H.; Schulz, P.; Heldin, C.H.; Miyazono, K. Cell (1993) 75.681-603 |
| #title | ing of a |
| #accession ##status ##molecule ##residues | A49432 preliminary type mRNA 1-503 ##label FRA |
| ##CIOSS- CIASSIFICATION KEYWORDS FEATURE | references obsinions #superfamily protein kinaue homology glycoprotein; phosphotransferase; transmembr |
| 203-499 SUMMARY | #domain protein kinase homology #label KIN #length 503 #molecular-weight 55959 #checksum 1518 |
| Query Match Best Local | 100.0%; Score 3687; DB 13; Length 503; Similarity 100.0%; Pred. No. 0.00e+00; 03. Conservative 0. Mismatrhes 0. Indels 0. Gans 0. |
| | |
| RESULT 2 ENTRY TITLE | JC2062 #type complete |
| Catanism | Mus musc; lus #common_name house mouse |
| CATE | -1994 #sequence_revision 27-Jun-1994 # ec-1995 |
| ACCESSIONS REFERENCE | |
| #authors #journal #title | A.; Shioda, N.; Maeda, T.; Tada, M.; Ue n. Biophys. Res. Commun. (1994) 198:1063- |
| | receptor for ligand binding. |
| #accession ##molecule ##residues | . JC2062 ule=type mRNA |
| CLASSIFICATION FEATURE | #superfamily protei |
| 1-19 20-499 | 01 |
| 122-145 | #label MAT\ #label MAT\ #domain transmembrane #status predicted #label TMM\ #domain profein kinase homology #label KIN\ |
| | #domain intraceilular kinase #la 340 #binding_site carbohydrate (Asn) |
| SUMMARY | predicted #length 499 #molecular-weight 55790 #checksum 157 |
| Query Match Best Local Matches 4 | h Similarity 96.4%; Pred. No. 0.00e+00; 485; Conservative 5; Mismatches 9; Indels 4; Gaps 1; |
| | aaaprrpqllivlvaaatllpgakalqcfchlctkdnftcetdglcfvsvte 56 |
| Qy 1 MEA | |
| Db 57 ttd | ttdkvihnsmeiaeidliprdrpfveapssktgavtttycengdhenkielpttekgsag 116 |
| Qy 61 TTD | TTDKVIHNSMCIAEIDLIPRDRPFVCAPSSKTGSVTTTYCCNQDHCNKIELPTTVKSSPG 120 |
| Db 117 1gp | 19pvelaaviagpvcfvcialmlmvyichnrtvihhrvpneedpsldrpfisegttlkdl |
| Dyi 771 dd | ivdnttaasasalullvartiartivlaesiakarfaevwrakwraeevavkifsereer 216 |

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177 lkdliydmttsgsgsglpllvgrtiartivlgesigkgrfgevwrgkwrgeevavkifss
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                                                                                                                                                                                                                                                                                                                                                                     transforming growth factor-beta type I receptor, ESK precursor - mouse
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#binding_site carbohydrate (Asn) (covalent)
predicted
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Pred. No. 0.00e+00;
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21-Jul-1995 #sequence_revision 28-Jul-1995 #text
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Noji, S.; Saito, T.
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Activin receptor-like kinases, A novel subclass of cell
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Massague, J.; O'Connor, M.B.
Mol. Cell. Biol. (1994) 14:944-950
Two distinct transmembrane serine/threonine kinases from
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08-Sep-1995 #sequence_revision 08-Sep-1995 #text_change
                                   301 tidiapnhrvgtkrymapevlddsinmkhfesfkradiyamglvfweiarrcsiggihed
                                                                       364 TIDIAPNHRVGTKRYMAPEVLDDSINMKHFESFKRADIYAMGLVFWEIARRCSIGGIHED
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rth 505 #molecular-weight 56806
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Mol. Cell. Biol. (1994) 14:3810-3821
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Miyazono, K.; Moren, A.; Grimsby, S.; Ichijo, H.; Heldin, C.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Characterization of type I receptors for transforming growth
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                                                                                                                                                                                                                                                       Gaps
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19-May-1994 #sequence_revision 19-May-1994 #text_change
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22 AAAAALLPGATALQCFCHL-CTKD--NFTCVTDGLCFVSVTET-TDKVIHNSMCIAEIDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ten Dijke, P. submitted to the EMBL Data Library, June 1993 ALK-3 and ALK-6: the closely related members in the
                                                                                                                                           #checksum 801
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                                                                                                                                                                                                                                                                                                                                                                                                                            activin receptor-like kinase 6 precursor - mouse
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                                                                                                               #label KIN
                                                                                                                                                                                                  Length 601;
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                                                                                                                                                                                                                                                     Indels
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                                                                                                                                                                                                                                                       77; Mismatches 111;
                                                                                                                                        #molecular-weight 67219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                #length 502 #molecular-weight 56944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 1793; DB 14;
Pred. No. 1.36e-287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            84; Mismatches 124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          #superfamily protein kinase homology
                                                     #superfamily protein kinase homology
                                                                                                                                                                                                  Score 2021; DB 12;
                                                                                                                                                                                                                            Pred. No. 0.00e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          M.; Miyazono, K.; Heldin, C.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Science (1994) 264:101-104
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                                                                                                                                                                                                                                                                                                                                                                                                   #type complete
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ##cross-references EMBL: Z23143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ##cross-references GB:Z23143
                           ##cross-references GB:U04692
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                                                                                                                                                                                                  54.8%;
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Best Local Similarity 54.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A53444; S40159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          266; Conservative
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483; Conservative Best Local Similarity DOMAIN NP BIND BINDING SEQUENCE P80204; SIGNAL DOMAIN CHAIN Matches Matches EG: OLT protein - protein database search, using Smith-Waterman algorithm 852.767 Million cell updates/sec 0.00e+00 0.00e+00 0.00e+00 0.00e+00 0.00e+00 0.00e+00 0.00e+00 0.00e+00 0.00e+00 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, 370 trvgtkrymppevldeslnrnhfqsyimadmysfglilweiarrcvsggiveeyqlpyhd 429 1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 251 TVMLRHENILGFIAADNKDNGTWTQLWLVSDYHEHGSLFDYIANRYTVTVEGMIKLALSTA 310 311 SGLAHLHMEIVGTQGKPAIAHRDLKSKNILVKKNGTCCIADLGLAVRHDSATDTIDIAPN 370 371 HRVGTKRYMAPEVLDDSINMKHFESFKRADIYAMGLVFWEIARRCSIGGIHEDYQLPYYD 430 430 lvpsdpsyedmreivcmkklrpsfpnrwssdeclrqmgklmtecwaqnpasrltalrvkk 489 431 LVPSDPSVEEMRKVVCEQKLRPNIPNRWQSCEALRVMAKIMRECWYANGAARLTALRIKK 490 1 MEAAVAAPRPRLLLLVLAAA......TALRIKKTLSQLSQQEGIKM 503 Pred. sglchlhteifstggkpaiahrdlksknilvkkngtcciadlglavkfisdtnevdippn MasPar time 12.51 Seconds SERINE/THREONINE-PROT SERINE/THREONINE-PROT SERINE/THREONINE-PROT SERINE/THREONINE-PROT SERINE/THREONINE-PROT SERINE/THREONINE-PROT SERINE/THREONINE-PROT and is derived by analysis of the total score distribution. SERINE/THREONINE-PROT SERINE/THREONINE-PROT SERINE/THREONINE-PROT ••• scale 0.584 = Description CREATED) LAST SEQUENCE UPDATE) LAST ANNOTATION UPDATE) Mean 50.633; Variance 86.716; 59021 segs, 21210388 residues (1-503) from US08436265.pep KIR4_HUMAN KIR4_RAT KIR2_HUMAN Tue Jun 24 18:00:22 1997; summaries HUMAN KIR6 MOUSE HUMAN MOUSE SUMMARIES CHICK HUMAN AL IGNMENTS RAT KIR1 RAT KIR5 F KIR6 KIR2 KIRS :: П >US-08-436-265-10 Listing first 45 ---Minimum Match 0% swiss-prot34 STANDARD; lar output not generated Query Match Length 502 502 532 532 509 490 tlakmsesgdikl 502 29, 29, 32, 491 TLSQLSQQEGIKM 503 PAM 150 Gap 11 (REL. (REL. (REL. 3687 100.0 68.4 68.2 48.6 48.6 48.0 47.8 44.8 LT 1 KIR4 HUMAN P36897; 01-JUN-1994 01-JUN-1994 01-NOV-1995 Post-processing: Perfect Score: Scoring table: 3687 3454 2552 2516 1793 1792 1762 1651 1646 Score Description: Statistics: MPsrch pp Sequence: Searched: Database: Run on: No. 1264597860 DA PP g ద à •à В g ð δ à

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-!- TISSUE SPECIFICITY: FOUND IN ALL TISSUES EXAMINED, MOST ABUNDANT
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PROSITE, PSO107; PROTEIN KINASE_ATP.
PROSITE, PSO1010; PROTEIN KINASE_ST.
PROSITE, PS50011; PROTEIN KINASE_DOM.
RECEPTOR; TRANSFERASE; SERINE/THREONINE-PROTEIN KINASE; ATP-BINDING;
TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                           -!- FUNCTION: TYPE I/TYPE II TGF-BETA RECEPTORS FORM AN HETEROMERIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DEV. DYN. 196:133-142(1993).
-!- FUNCTION: TYPE I/TYPE II TGF-BETA RECEPTORS FORM AN HETEROMERIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-1993 (REL. 27, CREATED)
61-OCT-1993 (REL. 27, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 24, LAST ANNOTATICT TRUBLE)
SERINE/THREONINE-PROTEIN KINASE RECEPTOR R4 PRECURSOR (EC 2.7.1.37)
SERINE/THREONINE-PROTEIN KINASE RECEPTOR R4 PRECURSOR (EC 2.7.1.37) (SKR4) (ACTIVIN RECEPTOR-LIKE KINASE 5) (ALK-5) (TGF-BETA TYPE I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- TISSUE SPECIFICITY: UROGENITAL RIDGE, TESTIS, OVARY, BRAIN AND
                                                                                                                                                                                                                                                                                                                                    COMPLEX AFTER BINDING TGF-BETA AT THE CELL SURFACE AND ACT AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPLEX AFTER BINDING TGF-BETA AT THE CELL SURFACE AND ACT AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SERINE/THREONINE KINASE RECEPTOR R4.
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SIMILARITY: WITH THE CONSERVED CATALYTIC DOMAINS OF SER/THR-
                                                                                                                                                                                                                                                                                                                                                                                                                                    IN PLACENTA AND LEAST ABUNDANT IN BRAIN AND HEART.
                                                                                               EUKARYOTA, METAZOA, CHORDATA, VERTEBRATA, TETRAPODA, MAMMALIA,
EUTHERIA, PRIMATES.
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بم
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cuerry Match 100.0%; Score 3687; DB 5; Length 503; Best Local Similarity 100.0%; Pred. No. 0.00e+00;
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                                                                                                                                                                                                                               FRANZEN P., TEN DIJKE P., ICHIJO H., YAMASHITA H., SCHULZ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
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Pred. No. 0.00e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=SPRAGUE-DAWLEY; TISSUE=UROGENITAL RIDGE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HE W.-W., GUSTAFSON M., HIROBE S., DONAHOE P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67D99EAB CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     55999 MW;
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95.3%;
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                                                                                                                                                                                                                                                           HELDIN C.H., MIYAZONO K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
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                                                                                                                                                                                                                                                                                    CELL 75:681-692(1993)
                                                                             HOMO SAPIENS (HUMAN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EUTHERIA; RODENTIA.
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CARBOHYD
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4,

Gaps

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5; Mismatches

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| K K K K K | PROSITE; PS500 RECEPTOR; TRAN TRANSMEMBRANE; | TE, F TOR; TEMBR | 11; SFER GLY | 1; PROTEIN KI PERASE; SERIN GLYCOPROTEIN; | . Z 🖂 | -PROTEIN | KINASE; ATP-BINDING | NDING; |
|------------------------------|---|------------------------|---|---|--|---|---|------------------------|
| FT FT FT | SIGNAL CHAIN DOMAIN TRANSMEM | JE Z | 1 24 127 | 23 505 126 149 | POTENTIAL. SERINE/THREON EXTRACELLULAR POTENTIAL. | NINE R (PO | KINASE RECEPTOR TENTIAL). | R2 . |
| FF | DOMAIN DOMAIN | 6 | 150 207 213 | 505 497 221 | CYTOPLASMIC (P. PROTEIN KINASE | (POTENT. SE. | AL) . | |
| FT | BINDING ACT SITE CARBOHYD | SITE | 3334 3354 335 | 33.4 43.5 83.5 | (BY SIMIL | SIMILARITY). ARITY. L. | | |
| රිදු | LICTENCE | CE | 505 AA; | 56806 | MM | F7 CRC32, | | |
| ŌĂĞ | Query Match Best Local Matches 3 | 1 Si 353 | Similarity 153; Conser | 68.4% 70.7% rvative | ; Score 2522; ; Pred. No. 0 62; Mismat | DB 5; .00e+00; ches 69; | Length 505; Indels 15; | Gaps 11; |
| MPsrch | dd los | prc | protein - p: | protein | database sea | search, using S | Smith-Waterman | algorithm |
| Run | ou: | | Tue Jun | n 24 18 | :01:25 1997; | MasPar time | 5.11 Seco | , |
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| Tit. Desc Perf Segu | Title: Description: Perfect Scor Sequence: | ı: ore: | >US-08-4 (1-503) 3687 1 MEAAVZ | -436-26) from VAAPRPR | 5-10 JS08436265.p LLLLVLAAA | | TALRIKKTLSQLSQQEGIKM | KM 503 |
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| Seal | Searched: | | 39797 | seds, 3 | 3636180 residue | sən | | |
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| Databa | abase: | | a-issued 1:51 2: 10:PCTS | ssued ::51 2:52 3 :0:PCT93 11 | :53 4:54 5:5 :PCT94 12:PC | 5 6:56 7:PCT T95 13:PCT96 | 90 8:PCT91 9 | :PCT92 |
| Stat | Statistics: | | Mean 33 | 3.610; | Variance 164 | .611; scal | e 0.204 | |
| | Pred. score and is | z b " | s the er th | umbe or anal | f results al to the s of the t | edicted by ore of the al score di | chance to have result being ; stribution. | ve a printed, |
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| ; | | ; | | 1 | - | Segmence | O. Applicati | |
| | | 4. 2 | 93.7 | | US-08-31 | Sequence 1 | 17, Applicati | 1.88e-288 |
| | | 17 | 68.3 | | PCT-US94- | Sequence 8 | Applicatio | 3.61e-206 |
| | | 181 | 67.3 | | US-08-143 | ч г | 5, Applicati | 5.17e-203 |
| | | 93 | 64.7 48.6 | | US-08-341 PCT-US95- | ∾ ∞ | , Applicatio | 1.63e-194 7.87e-143 |
| | 9 17 | 1785 | 48.4 | 502 11 532 11 ALIGN | PCT-US94 PCT-US94 AENTS | 4.0 | Applicati Applicati | 3.93e-142 9.77e-141 |
| RESULT ID P | JLT 1 PCT-US! | 94 | -10080-10 | STA | STANDARD; PI | PRT; 503 AA | | |
| XX AC | XXXXXX | | | | | | | |

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417 IGGIHEDYQLPYYDLVPSDPSVEEMRKVVCEQKLRPNIPNRWQSCEALRVMAKIMRECWY 476
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                                                                                                                                                                                                                                                                                                                                                        REERSWFREAEIYQTVMLRHENILGFIAADNKDNGTWTQLWLVSDYHEHGSLFDYLNRYT 296
                                                                                                          TTDKVIHNSMCIAEIDLIPRDRPFVCAPSSKTGAVT--YCCNQDHCNKIELPTTGPFSEK 114
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                                                                                                                            TIDKVIHNSMCIAEIDLIPRDRPFVCAPSSKTGSVTTTYCCNQDHCNKIELPTT---V-K
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                                     MEAASAALRRCLLLIVLVAAAT ----LLPGAKALQCFCHLCTKDNFTCETDGLCFVSVTE
                                                                        MEAAVAAPRPRIJILIVLAAAAAAAALILPGATALQCFCHLCTKDNFTCVTDGLCFVSVTE
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                                                                                                                                                                                                 Sequence 17, Application US/08149105
Patent No. 5538892
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      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-149-105-17
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PCT-US94-10080-8
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      483;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: FOUR NOVEL RECEPTORS OF THE TGF-B CITLES OF INVENTION: FAMILY NUMBER OF SEQUENCES: 17
                                                                                                                                                                                               Indels
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Pred. No. 1.88e-288;
                                                                                                                                                             94.7%; Score 3493; DB 11; 95.7%; Pred. No. 7.01e-292;
                                                                                                                                                                                                                                                                      501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER REALABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50Z or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              00786/127002
                                                                                                                                                                                                 5; Mismatches
                                                                     Sequence 10, Application PC/TUS9410080 GENERAL INFORMATION:
APPLICANT: GENETICS INSTITUTE, INC.
TITLE OF INVENTION: RECEPTOR PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/317,847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    501 AA, 55999 MW, 1252583 CN,
                                                                                                                                                                                                                                                                     PRT;
                                    Sequence 10, Application PC/TUS9410080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: March 11, 1993
APPLICATION NUMBER: 07/853,396
FILING DATE: March 18, 1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08/029,673
                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 17, Application US/08317847
                                                                                                                                                                                                                                                                                                                                                                         Sequence 17, Application US/08317847.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Donahoe, Patricia K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fish & Richardson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Clark, Paul T. REGISTRATION NUMBER: 30,162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Gustafson, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (617) 542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
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INFORMATION FOR SEQ ID NO:
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95.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: Massachusetts
                                                                                                                                                                             Best Local Similarity 95.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    He, Wei W.
                                                                                                                                                                                               Conservative
                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: U.S.A. ZIP: 02110-2804
                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                               Patent No. 5547854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
                                                                                                                                                                                                                                                                     US-08-317-847-17
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                                                                                                                                                                                                 485;
01-JAN-1900
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Gaps

116 174 176 234 236

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356

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354

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Matches

RESULT

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APPLICANT: J_rnvall, Henrik
TITLE OF INVENTION: A No. 5614609el Serine Threonine Kinase Receptor
NUMBER OF SEQUENCES: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NKDNGTWTQLWLVSEYHEQGSLYDYLNRNIVTVAGMVKLALSIASCLAHLHMEIVGTQGK 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N--NVTKTECCFTDFCNNITLHLPTASPDAPRLGPTELTVVITVPVCLLSIAAMLTIWAC 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         137 QDRQCTYRKTKRHNVEEPLAEYSLVNAGKTLKDLIYDATASGSGSGLPLLVQRTIARTIV 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LQEIVGKGRFGEVWHGRWCGEDVAVKIFSSRDERSWFREAEIYQTVMLRHENILGFIAAD 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31 ATALQCFCHLCTKDNFTCVTDGLCFVSVTETTDKVIHNSMCIAEIDLIPRDRPFVCAPSS
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                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                65; Mismatches 76;
                                                                           ADDRESSEE: Sterne, Kessler, Goldstein & STREET: 1100 New York Avenue, Suite 600
                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 1459.0230001
                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
HENCE 493 AA, 54800 MW; 1225231 CN;
                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/341,916
FILING DATE: Herewith
                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                            29,021
                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION
    NAME: Goldstein, Jorge A
                                                                                                                                                                MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                (202)371-2600
   Ib ez, Carlos
Ryd n, Mikael
                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 493 amino anics
                                                                                                                                                                                                                                                                                                                                         (202)371-2540
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                                                                                                                                                                                                                CURRENT APPLICATION DATA:
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Best Local Similarity 68.3%;
                                                                                                                                                   COMPUTER READABLE FORM:
                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                325; Conservative
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                                                                                                   CITY: Washington
STATE: DC
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                                                                                                                             USA
                                                                                                                                        ZIP: 20005
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               APPLICANT:
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                                                                            Score 2481; DB 5; Length 501;
Pred. No. 5.17e-203;
                                                                                                    60; Mismatches 67; Indels
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Patent No. 5547854
                                                   Sequence 15, Application US/08149105
                         Sequence 15, Application US/08149105.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 15, Application US/08317847
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Patent No. 5614609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/08341916
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                                                               Patent No. 5538892
                                                                                        Best Local Similarity
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Indels

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436

446

n.a. database search, using Smith-Waterman algorithm n.a. MPsrch_nn

1344.779 Million cell updates/sec MasPar time 1614.00 Seconds Thu Jun 26 01:48:57 1997; Run on:

Tabular output not generated.

>US-08-436-265-17 (1-1952) from US08436265.seq 1952 Title:

Perfect Score: Description:

......CCATTTTTTAAAAAAA 1952 ITCGCCGCCGTCTTCAACGG.......GGTAAAAAAAATATTTTTT 1 AAGCGGCGGCAGAAGTTGCC. Seguence:

TABLE default Gap 6 Scoring table:

Dbase 0; Query 0 ٠. STD Nmatch 333249 segs, 555961234 bases x 2 Searcned:

processing:

summaries Listing first 45 Minimum Match 0%

embi-newll Database:

1:BCT 2:FUN 3:GEN 4:HUM1 5:HUM2 6:HUM3 7:INV1 8:INV2 9:INV3 10:INV4 11:INV5 12:INV6 13:INV7 14:ORG 15:MAM 16.VRT 17:PLN 18:PRO1 19:PRO2 20:ROD 21:SYN 22:UNC 22:VIP: 24:VIR2

genbank97 Detabaso:

60:PLN4 61:PLN5 62:PLN6 63:PLN7 64:PLN8 65:PLN9 66:PLN10 67:PRI1 68:PRI2 69:PRI3 70:PRI4 71:PRI5 72:PRI6 73:PRI7 74:PRI8 75:PRIS 76:PRI10 77:PRI11 78:PRI12 79:PRI13 46:MAM1 47:MAM2 4 53:PAT2 54:PAT3 5 60:PLN4 61:PLN5 6 200

80:PRI14 81:ROD1 82:ROD2 83:ROD3 84:ROD4 85:ROD5 86:ROD6 87:ROD7 88:RODE 89:STK 90:SYN 91:UNA 92:VRL1 93:VRL2 94:VRL3 95:VRL4 96:VRL5 97:VRL6 96:VRL7 99:VRL8 100:VRL9 genbank-new11

Database:

101:BCT 102:GEN 103:INV1 104:INV2 105:MAM 106:VRT 107:PHG 108:PLN 109:PRI1 110:PRI2 111:ROD 112:SYN 113:UNA 114:VRL

Mean 11.866; Variance 4.400; scale 2.697 Statistics:

115:part1 116:part2

Database:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| | | Description Pred. No. | M.musculus ALK-6 mRNA 0.00e+00 | Chicken mRNA for rece 0.00e+00 | Rat mRNA for bone mer 0.00e+00 | bone morphogenetic pr 0.00e+00 | Rat mRNA for bone mor 0.00e+00 | Rat mRNA for bone mor 0.00e+00 | bone morphogenetic pr 0.00e+00 | M.musculus ALK-3 mRNA 0.00e+00 | Mouse mRNA for BMP re 0.00e+00 | Mus musculus type I r 0.00e+00 | |
|---|--------|-----------------------|--------------------------------|--------------------------------|--------------------------------|--------------------------------|--------------------------------|--------------------------------|--------------------------------|--------------------------------|--------------------------------|--------------------------------|--------------|
| | | 3 ID | MMALK6A | CHKRPK1 | RATRB4R1 | 0, | RNRALK3 | ш, | 8 \$75359 | MMALK3A | I MUSBMPRC | MMU04672 | ALTC NIMENTS |
| | í | E : | 81 | 49 | 87 | 20 | 20 | 87 | 88 | 81 | 84 | 82 | |
| | - | Match Length DB | 1944 81 | 2252 | 1599 | 2620 | 3003 | 3003 | 3167 | 1599 | 2292 | 2402 | |
| % | Query | Match | 99.6 | 47.8 | 27.4 | 27.4 | 27.4 | 27.4 | 27.4 | 26.6 | 26.6 | 26.6 | |
| | | | | | | | | | | | _ | _ | |
| | | Score | 1944 | 93. | 534 | 535 | 536 | 535 | 53.5 | 515 | 520 | 52(| |
| | Result | NO. | - | N | ጠ | 4, | យា | 10 | 7 | , no | χI | 1.0 | |

Eukaryotae, mitochondrial eukaryotes, Metazoa, Chordata, Vertebrata; Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae, Gallus.

Unpublished (1992)

1 (sites)
Nohno, T.

REFERENCE AUTHORS JOURNAL

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morphogen; agonist; antagonist; chimeric receptor; gene therapy; ss.
                          ALK-6; OP1 binding receptor; osteogenic protein 1; morphogenesis;
                                                                                                                                                                                                                                                                                                                        serine threonine kinases, activin meceptors, Act-R, superfamily, the sforming growth factor, TGF, miagnistics, detection, therapy, rheumatoid arthritis, glomerular negimitis, fibrosis, ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bone morphogenic protein; receptor; serine/threonine kinase; BMP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence encoding bone morphogenic protein receptor CFK1-43a.
                                                                                                                                                                                                                                                                                                             Mouse Activin receptor-like kinase 6 (mALK-6) cDNA.
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Pred. No. 0.00e+00;
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                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "contains an in-frame stop codon at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product= activin receptor-like kinase
                                                                  Location/Qualifiers
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                                                                                                                                                                                                                               (CREA-) CREATIVE BIOMOLECULES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-OCT-1993; GB-021344. (LUDW-) LUDWIG INST CANCER RES.
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Q83531 standard; DNA; 2076 BP.
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Q66642 standard; cDNA; 1952
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                                                                                                                                                                                                                29-APR-1994; US-236428
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                                                                                                                                                             'product= mouse ALK-6
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                                                                                                                                                                                                    28-APR-1995; U05467
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 13-FEB-1996 (fir:
Mouse ALK-6 cDNA.
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  Sumitomo,S., Saito,T. and Nohno,T. A new receptor protein kinase from chick embryo related to type II
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                                                                                                                                                                                                                                                                   Thu Jun 26 02:16:28 1997; MasPar time 188.32 Seconds 958.907 Million cell updates/sec
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                                                                                                                                                                                       Score 933; DB 49; Length 2252;
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                                                                              Submitted (20-OCT-1992) to DDBJ by: Tsutomu Nohno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mouse ALK-6 cDNA.
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                                                   DNA Sequence 3, 297-302 (1993)
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Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
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Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
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                           1819 AGGAACCCAGAAACACGGATTCATCATGGCTTTCTGAGGAGGAGAAACTGTTTGGGTAAC 1878
                                                          1940 tigiticaagalatgaatgcatgiticettictaagaaageeetgtatittgggattaeeati 1999
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Vertebrata, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
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                                                                                                                                                                                                                                                                                         This clone is available royalty-free through LLNL , contact the {\tt IMAGE} Consortium (info@image.llnl.gov) for further information.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Vector: pT7T3D (Pharmacia) with a modified
                                                                                                                                                                             4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
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Washington University School of MedicineP
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                                                                                      Contact: Marra M/Mouse EST Project
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                                                                                                                                                                                                                                                                   Email: mouseest@watson.wustl.edu
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| g | 2(| 201 TAAP | AGGAGC | CAACTCGGCC | CATA | AGTGAC-AGAG | SAAGTTCGTTG | ATA | TAAAGGAGCAACTCGGCCATAAGTGAC-AGAGAAGTTCGTTGATAACATGCTCTACGAA | GAA 259 | |
| ò | 1, | 140 TAAA | AGGAGC | NA CCCGGCCAT | CATA | AGTGAAGAGAG | SAAGTTTATTG2 | ATA | | :GAA 199 | |
| g | 2(| 260 GCTC | CTGGAA | AAATTAAATC | GTGG | GCACCAAGAAG | SGAGGATGGTG | AGAC | GCTCTGGAAAATTAAATGTGGGCACCAAGAAGGAGGATGGTGAGAGTACAGCCCCCACTG | CTG 319 | |
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| Q | 3, | 320 CTC | BGCCCA | AAGGTCCTG | CGTT | GTAAATGCCAC | CACCACTGTC | CTG2 | CTCGGCCCAAGGTCCTGCGTTGTAAATGCCACCACCACCACTGTCCTGAAGACTCAGTCAACA | ACA 379 | |
| ζζ | 56 | 60 CTC | 3GCCCA | AAGATCCTA(| CGTT | GTAAATGCCAC | CACCACTGTC | 7990 CGG7 | TGGGCCCAAGATCCTACGTTGTAAATGCCACCACCACTGTCGGGAAGACTCAGTCAACA | ACA 319 | |
| පු | 38 | 380 ATAT | TCTGCA | AGCACAGATO | 36GT | ACTGCTTCAC | SATGATAGAAG | AAG? | ATATCTGCAGCACAGATGGCTACTGCTTCACGATGATAGAAGAAGACGACTCTGGAACGC | CGC 439 | |
| ŏ | 3; | 320 ATAT | rctgca | AGCACAGATO | 36GT | ACTGCTTCACG | atgatagaag) | AAG? | ATAICTGCAGCACAGATGGGTACTGCTTCACGATGATAGAAGAAGAAGATGACTCTGGAATGC | 11 TGC 379 | |

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ALK-3; OP1 binding receptor; osteogenic protein 1; morphogenesis;
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28-MAY-1993; GB-011047.
02-JUL-1993; GB-013763.
03-AUG-1993; GB-016099.
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28-APR-1995; U05467
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17-NOV-1993; C
17-NOV-1992; C
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05-JUN-1995; US-462467.
                                                                                Rosenbaum JS;
                       17-MAY-1996.
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                                                                                                                                       serine/threonine kinase receptors may be used in compositions to inhibit the effects of BMP's such as BMP-2 and BMP-4. The truncated receptors pref. comprise the ligand binding domain, but not the serine/three...e kinase and transmembrane domains. The 'runcated proteins are soluble and will be excreted into supernatic by
                                                                                                                                                                                                                                                                                                                    mlirssykinvytkkedgestaptarpkvlrckchhhcpedsvnnicstdgycftmieed 60
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BMP type II receptor kinase-3; BRK-3; bone morphogenetic protein;
BMP type I receptor kinase; BRK-2; BMP receptor.
                                                                                                                                                                                                           delivered in a medium or matrix which partially impedes their mobility, thereby localising the cells to a site of bone or cartilage injury.
                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                  recombinant mammalian cells expressing them. Such cells can
                                                                                                                                                                                                                                                                       Score 3711; DB 13; Length 502; Pred. No. 0.00e+00;
                                                                                          proteins
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                                                                                                                 Claim 17; Page 54-55; 83pp, English.
Truncated bone morphogenic protein (BMP) receptors and
                                                                                           Truncated BMP and serine/threonine kinase receptor
                                                                                                      used to inhibit the effects of BMP-2 and/or BMP-4.
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                                                         Yamaji N;
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                                                      Celeste AJ, Thies RS, Wozney JM, WPI; 95-131350/17.
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31-DEC-1996 (first entry)
                                            (GEMY ) GENETICS INST INC
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                     07-SEP-1994; U10080.
17-SEP-1993; US-123934.
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                                                                                                                                                                                                                                                                                                                      BMP
                                                                                                                                                                                                                                                                                                                                   receptor affinity or for determining the concentration of a BMP receptor ligand in a clinical sample. The complex can be expressed by host cells co-transfected with vectors carrying the appropriate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                    BMP type I receptor kinase protein and BMP receptor kinase protein
                                                                                                                                         Full-length chick bone morphogenetic protein (BMP) type I receptor kinasa protein-2 (BRK-2) (R95226) is a receptor capable of binding BMP and cransducing a signal initiated by the binding. Its amino acid sequence was deduced from a cDNA clone (T28022). A BMP
                                                                                                                                                                                                            receptor kinase protein complex formed of full-length, incomplete or soluble BMP type I receptor kinase protein and full-length, incomplete or soluble BMP type II receptor kinase. 3 (BRK-3) (see also %#5222-25 and R95227-34) is useful for screening cpds. for BM receptor affinity or for determining the contraction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       wfretelyqtvlmrhenilgflaadikgtgswtqlylitdyhengslydylksttldtkg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tisssklsmesrkedsegtapappqkkiscqchhhcpedsvnstcstdgycftileed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MLLRSSGKLNVGTKKEDGESTAPTPRPKILRCKCHHHCPEDSVNNICSTDGYCFTMIEED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gnihhkallisvtvcsillvliiifcyfrykrqearprysiglegdetyippgeslkdli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 eqsqssgsgsglpllvqrtiakqiqmvkqigkgrygevwmgkwrgekvavkvfftteeas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EQSQSSGSGSGLPLLVQRTIAKQIQMVKQIGKGRYGEVWMGKWRGEKVAVKVFFTTEEAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              eeyqlpyhdlvpsdpsyedmreivcikrlrpsfpnrwssdeclrqmgklmmecwahnpas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 502;
                                                     using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23; Mismatches 19; Indels
                                                 activities
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 3466; DB 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 0.00e+00;
                                                 protein
                                                                                                                    Claim 2; Page 70-71; 101pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                              DNA sequences (see also T28018-30)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            502
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                                             Assays for bone morphogenetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 91.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rltalrvkktlakmsesgdikl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   460; Conservative
WPI; 96-251887/25.
                       N-PSDB; T28022.
                                                                                                                                                                                                                                                                                                                                                                                                                                      CONTRACTOR
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standard; Protein;

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screening; reporter gene; bone morphogenetic protein-antagonist; tΩ Bone morphogenetic protein type-I receptor kinase-2. Chicken, bone morphogenetic protein receptor kinase-2; bone morphogenetic protein receptor kinase-3; antibody; diagnostic; bone disorder; osteogenic; bone morphogenetic protein-agonist; The BRK-3 receptor and antibodies against genes, followed by screening with an antibody generated against an intracellular kinase peptide sequence present in BRK-1. BRK-2 used contains an SGSGSG motif in the juxtamembrane region, 35-40 amino " ' smembrane region, and the C-terminus region is cysteine residues (cysteine box) within 25-30 amino acids of the the sequence represents chicken bone morphogenetic protein (BMP) differentiation 1, response to BMP. Complex formation whomeen BRK-2 and type-II BRK-3 may be studied by co-expression of both trnasmembrane region, and an upstream cysteine box after the ...e extracellular domain contains a clustir of Isolated bons marphogenic protein receptor kinase protein determine if a tert cpd. is capable of binding to, or is (ant)agonist of BMP receptor kinase protein transcription Example 4; Page 67-68; 87pp; English. receptor type-I kinase-2 (BRK-1), which induces cellular Location/Qualifiers 'note= "Conserved BRK-2 motif" (PROC) PROCTER & SAMBLE CO. hormone-responsive element putative signal peptide. 186..191 Rosenbaum JS; 04-NOV-1994; US-3:1179. 30-OCT-1995; U14085 Gallus domesticus WPI; 96-251762/25 N-PSDB; T27229. acids from . WO9614412-A2. 17-MAY-1996. 22-AUG-1996 very short. Nohno T, Peptide drug Key

Gaps . 0 Length 502; Score 3466; DB 17; Length 5 Pred. No. 0.00e+00; 23; Mismatches 19; Indels 92.7%; 91.6%; 460; Conservative Best Local Similarity Query Match Matches

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61 dsgghlvtkgclglegsdfqcrdtpiphqrrsiecctgqdycnkhlhptlpplknrdfae 120 ÎÎÎ

61 DSGMPVVTSGCLGLEGSDFQCRDTPIPHQRRSIECCTERNECNKDLHPTLPPLKDRDFVD 120 gnihhkallisvtvcsillvliiifcyfrykrqearprysigleqdetyippgeslkdli 121

δ g ò

181 EQSQSSGSGLPLLVQRTIAKQIQMVKQIGKGRYGEVWMGKWRGEKVAVKVFFTTEEAS egsgssgsgsglpllvgrtiakgigmvkgigkgrygevwmgkwrgekvavkvfftteeas 181 g à

241 WFRETEIYQTVLMRHENILGFIAADIKGTGSWTQLYLITDYHENGSLYDYLKSTTLDAKS wfretelyqtvlmrhenilgflaadikgtgswtqlylitdyhengslydylksttldtkg 241 g ò

엄 ò

480 EEYQLPYHDLVPSDPSYEDMREIVCMKKLRPSFPNRWSSDECLROMGKLMTECWAQNPAS 480 eeyqlpyhdlvpsdpsyedmreivcikrlrpsfpnrwssdeclrqmgklmmecwahnpas ALK-3; OP1 binding receptor; osteogenic protein 1; morphogenesis; Location/Qualifiers Æ rltalrvkktlakmsesqdikl 502 502 morphogen; agonist; antagonist. T 6 R85207 standard; Protein; 532 RLTALRVKKTLAKMSESQDIKL 13-FES-7996 (first entry) 24..152 . . 23 'label= Sig_peptide Homo sapiens Human ALK-3 R85207; Peptide Domain 421 481 481 361 421 Key RESULT 용 8 ò g à à

Identifying osteogenic protein-1 receptor-binding analogue - usefui in the design of morphogen agonists and antagonists for therapeutic The Type-I cell surface receptors ALK-2, ALK-3 and ALK-6 (given R85206, R85207 and R85209) have specific binding affinity for osteogenic protein 1 (OP1) and OP1-related analogues. The receptors are used to identify novel morphogen receptor binding diagnostic and experimental purposes Claim 1; Page 68-71; 95pp; English. analogues useful in drug design. N-PSDB; T06031. Sequence

Sampath KT;

Miyazano K,

(CREA-) CREATIVE BIOMOLECULES INC.

28-APR-1995; U05467. 29-APR-1994; US-236428.

(LUDW-) LUDWIG INST CANCER RES.

Dijke PT, Heldin C,

therapy to bind or scavenge BMPs. In addition, expression of the

it may be used in diagnostic assays for BMP disorders, or in BRK-3 gené along with a reporter gene under the control of a compounds for BRK-agonist or -antagonist activity, by monitoring

reporter gene expression.

- 502 AA;

Sequence

hormone- responsive element in a cell culture may be used to

WPI; 95-393076/50.

domain"

/note= "serine/threonine-kinase

7.7

MO9E300W

.3651-NON-1995.

/label= Intracellular domain

/labeas Transmembrane domain /label= Extracellular_domain

Dorr ...

236..527

Domain

Gaps ŭ, Score 2757; DB 14; Length 532; Pred. No. 3.32e-259; Indels 76; Mismatches 61; Query Match 73.7%; Best Local Similarity 71.9%; 363; Conservative Matches

29 mlhgtgmksdsdqkksengvtlapedtlpflkcycsghcpddainntcitnghcfaiiee

5

59

147 119 ddqgettlasgcmkyegsdfqckdspkaqlrrtieccrt-nlcnqylqptlppvvigpff DDSGMPVVTSGCLGLEGSDFQCRDTPIPHQRRSIECCTERNECNKDLHPTLPPLKDRDFV :: :: 89 9

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240

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g à 267 dlidqsqssgsgsglpllvqrtiakqiqmvrqvgkgrygevwmgkwrgekvavkvfftte 120 208 엄

dgsirwlvllismavciiamiifsscfcykhycksissrrrynrdlegdeafipvgeslk

148

300

300

207

easwfreteiygtvlmrhenilgfiaadikgtgswtqlylitdyhengslydflkcatld 327 268

DLIEQSQSSGSGSGLPLLVQRTIAKQIQMVKQIGKGRYGEVWMGKWRGEKVAVKVFFTTE

178

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H.; Heldin, C.;
                                                                                                                             growth
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predicted
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 19-May-1994 #sequence_revision 19-May-1994 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            #formal_name Rattus norvegicus #common_name Norway rat
22-Apr-1995 #sequence_revision 26-May-1995 #text_change
                                                                                                                          transforming
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   #checksum 5099
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yamaji, N.; Celeste, A.J.; Thies, R.S.; Song, J.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  S.M.; Goltzman, D.; Lyons, K.M.; Nove, J.; Rosen,
                                                                                                                                                                                                                                                                                                                      ALK-3 and ALK-6: the closely related members in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Biochem. Biophys. Res. Commun. (1994) 205:1944-1951
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 #domain protein kinase homology #label KIN
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receptor protein kinase RPK-1 precursor - chicke
#formal_name Gallus gallus #common_name chicken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 3740; DB 14; Length book
Pred. No. 0.00e+00;:
                                                                                                                                                                                                                                                                   Miyazono, K.; Moren, A.; Grimsby, S.; Ichijo,
                                                                                                                                                                                                                                                                                   ten Dijke, P.
submitted to the EMBL Data Library, June 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 #region protein kinase ATP-binding motif^
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                                                                                                                                                                                                                                                                                                                                       serine/threonine kinase receptor family
                                                                                                                      Characterization of type I receptors for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         serine/threonine kinase receptor - rat
                                                                     ten Dijke, P.; Yamashita, H.; Ichijo,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   #length 502 #molecular-weight 56944
                                                                                                                                                                                                                                                                                                                                                                                                                                              #superfamily protein kinase homolog;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            #superfamily protein kinase homology
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Best Local Similarity 99.0%; Pred. No. 0.00e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               glycoprotein; transmembrane protein
                                                                                     M.; Miyazono, K.; Heldin, C.H.
Science (1994) 264:101-104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3; Mismatches
                                                                                                                                         factor-beta and activin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           #type complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      binds BMP-2 and BMP-4.
                                                                                                                                                                                                                                                                                                                                                                                                          1-502 ##label MIY
                                                                                                                                                                                                             1-502 ##label TEN
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                                                                                                                                                                                                                                                                                                                                                                                                                           ##cross-references EMBL: Z23143
                                                                                                                                                                                                                               ##cross-references GB:Z23143
                                                                                                                                                                           preliminary
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                                  A53444; S40159
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                   08-Dec-1995
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                                                                                                                                                                                            ##molecule_type mRNA
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ORGANISM
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 DATE
                                                                                                                                                                                                                                                                                                                                                       protein - protein database search, using Smith-Wederman algorithm
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                                                                                                                          447
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                   297
                                                                     298 AKSMLKLAYSSVSGLCHLHTEIFSTQGKPAIAHRDLKSKNILVKKNGTCCIADLGLAVKF 357
                                                                                                                                        358 ISDINEVDIPPNTRVGTKRYMPPEVLDESLNRNHFQSYIMADMYSFGLILMEIARRCVSG 417
                                                                                                                                                                                                             1:ann1 2:ann2 3:ann3 4:ann4 5:unann1 6:unann2 7:unann3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MIJESSGKINVGTKKEDGES.....TALRVKKTLAKMSESQDIKL 502
238 BASWFRETEIYQTVLMRHENILGFIAADIKGTGSWTQLYLITDYHENGSLYDYLKSTTLD
                                                    328 trallklaysaacglchlhteiygtqgkpaiahrdlksknilikkngscciadlglavkf
                                                                                                                          nsdtnevdvplntrvgtkrymapevldeslnknhfqpyimadiysfgliiwemarrcitg
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activin receptor-like kinase 6 precursor - mouse
#formal_name Mus musculus #common_name house mouse
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ALK-3 protein - huma
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  colvin receptor-like kinases: a novel subclass of cell-surface receptors with predicted serine/threonine finase activity.
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                                                                                                                                                                                       76; Mismatches 61; Indels
                                                                                                      ##residues 1-532 ##label RES
##cross-references EMBL:222535; NID:9402186; CDS
X #length 532 #molecular-weight 60201
                                                                                                                                                              Score 2757; DB 13;
Pred. No. 0.00e+00;
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                                                                                                                                                                                                                                KIN
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Pred. No. 0.00e+00;
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                                                                                        A new receptor protein kinase from type II receptor for IGF-beta. A56683
                                                                 S.; Saito, T.; Nohno,
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Gaps

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PID:9402187 #checksum Length 532,

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GB/EMBL/DDBJ

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1:partl 2:part2 3:part3 4:part4 5:part5 6:part6 7:part78:part8 9:part9 10:part10 11:part11

SERINE/THREONINE KINASE RECEPTOR

EXTRACELLULAR (POTENTIAL)

POTENTIAL.

13 502 126 148 502 494

TRANSMEM

SIGNAL DOMAIN DOMAIN DOMAIN

CHAIN

1 14 127 127 204 231 332

CYTOPLASMIC (POTENTIAL)

PROTEIN KINASE

(BY SIMILARITY)
(BY SIMILARITY)

ATP

231

MW; D404D2DB CRC32;

56766

502 AA;

SEQUENCE

ACT_SITE CARBOHYD

NP BIND BINDING

BY SIMILARITY. POTENTIAL.

scale 0.580 Mean 50.508; Variance 87.156; Statistics:

chance to have a result being printed, Pred. No. is the number of results predicted by chance to score greater than or equal to the score of the result bein and is derived by analysis of the total score distribution

SUMMARIES

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|--------|----------|-------------|-----------------------------|-----------|----------|----------------------------------|---|---------|
| Result | ılt | | Query | | | | | |
| Z | No. | Score | Match I | Length | DB | ID | Description | Pred. N |
| ! ! | | 3740 | 100.0 | 502 | i us | XIR6 MOUSE | SERINE/THREONINE-PROT | 0.00e+C |
| | 7 | 3466 | 92.7 | 502 | Ŋ | KIR6 CHICK | SEKINE/THREONINE-PROT | 0.00e+0 |
| | m | 2757 | 73.7 | 532 | Ŋ | KIRS HUMAN | SERINE/THREONINE-PROT | 0.00e+C |
| | 4 | 2756 | 73.7 | 532 | Ŋ | KIR5 MOUSE | SERINE/THREONINE-PROT | 0.00e+C |
| | Ŋ | 1842 | 49.3 | 501 | Ŋ | KIR4 RAT | SERINE/THREONINE-PROT | 0.00e+C |
| | φ | 1793 | 47.9 | 503 | Ŋ | KIR4_HUMAN | SERINE/THREONINE-PROT | 0.00e+C |
| | 7 | 1700 | 45.5 | α: ξ | Ŋ | KIR2 HUMAN | SERINE/THREONINE-PROT | 0.00e+C |
| | œ | 1696 | 45.3 | 505 | Ŋ | KIR2 RAT | SERINE/THREONINE-PROT | 0.00e+C |
| | 6 | 1679 | 44.9 | 509 | Ŋ | KIR1 HUMAN | SERINE/THREONINE-PROT | 0.00e+C |
| | 9 | 1669 | 44.6 | 509 | D. | KIR1_RAT | SERINE/THREONINE-PROT | 0.00e+C |
| tr. | Į. | - | | | | | | |
| ᄗ | <u>7</u> | KIR6 MOUSE | | SELECTED! | :: | PRT; 5 | 502 AA. | |
| AC | P3(| P36898; | | | | | | |
| DŢ | 01 | 01-JUN-1994 | 94 (REL. | 29, | CREATED) | TED) | | |
| DI | 0.1 | 01-JUN-1994 | | 29, | LAST | SEQUENCE UPDATE) | OATE) | |
| DI | 01 | 01-NOV-1995 | 95 (REL. | | AST | LAST ANNOTATION UPDATE) | | |
| DE | SE | RINE/TH | REONINE. | VIE | M M | INASE RECEPT | RE FRECURSOR : | .1.37) |
| D | (S | (SKP6) (À | CLIVIN 1 | 五十二五 | iR-L | (ACTIVIN FELT TOR-LIKE KINASE 6) | (ALK-6). | |
| SO | M | S MUSCO | MUS MUSCULUS (MOUSE) | JSE) . | | | | |
| ပ္ပ | EU | KARYOTA | EUKARYOTA; METAZOA; | |)RDA | TA; VERTEBRA | CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA; | |
| ပ | EO | THERIA; | EUTHERIA, RODENTIA | [A. | | | | |
| S. | Ξ, | | | | | | | |
| RP | SE | QUENCE | SEQUENCE FROM N.A. | .; | | | | |
| RX | MΕ | MEDLINE; | 94188705. | | | | | |
| K.A | ΞE | N DIJKE | TEN DIJKE P., YAMASHITA H., | AASHIT? | щ | , ICHIJO H., | FRANZEN P., LAIHO M., | |
| RA. | Z. | YAZONO | MIYAZONO K., HELDIN | DIN C.H.; | | | | |
| 2 | SS | SCIENCE 2 | 264:101-104(1994) | 104 (199 | . (1) | | | |
| ပ္ပ | 1 | - SUBCE | SUBCELLULAR LOCATION: | COCATIC | N | TYPE I MEMBRANE PROTEIN | NE PROTEIN. | |
| ပ္ပ | 1 | i | SIMILARITY: WITH | | Ö | ONSERVED CAT | THE CONSERVED CATALYTIC DOMAINS OF SER/THR- | HR- |
| ည | | PROTE | PROTEIN KINASES. | | STRONG, | | TO ACTIVIN RECEPTORS. | |
| DR | ü | | ٠. | G437871; | ï | | | |
| DR | Ы | | | 144. | | | | |
| DR | PIR; | C) | 59; \$40159 | 159. | | | | |
| 105 | HS | HSSP; P01 | P01359; 1PCP | ζ₽. | | | | |
| | = | | | | | | | |
| RE | E | 2 | | | | | | |
| ID | KI | KIR6 CHICK | | STANDARD; | | PRT; 5 | 502 AA. | |

EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; AVES; NEOGNATHAE 01-OCT-1996 (REL. 34, CREATED)
01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
SERINE/THREONINE-PROTEIN KINASE RECEPTOR R6 PRECURSOR (EC 2.7.1.37)
(SKR6) (ACTIVIN RECEPTOR-LIKE KINASE 6) (ALK-6) (RPK-1). 502 AA. STANDARD; GALLUS GALLUS (CHICKEN) GALLIFORMES KIR6_CHICK Q05438;

SEQUENCE FROM N.A.
MEDLINE, 94003400.
YAMAZAKI Y., SAITO T., NOHNO T.,
DNA SEQ. 3:297-302(1993).

SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
SIMILARITY: WITH THE CONSERVED CATALYTIC DOMAINS OF SER/THR-PROTEIN KINASES. STRONG, TO ACTIVIN RECEPTORS. ---

EMBL; D13432; G222863; -. RECEPTOR; TRANSFERASE; SERINE/THREONINE-PROTEIN KINASE; ATP-BINDING;

TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.

ם . SCHULZ P., SARAS MEDLINE; 93390967. TEN DIJKE P., ICHIJO H., FRANZEN P., SCH TOYOSHIMA H., HELDIN C.H., MIYAZONO K.; SEQUENCE FROM N.A. TISSUE=PLACENTA; RESULT
11D KII
AC P3 OT
DT 011
DT 011
DT 011
DE (SE OC)
CC EU
CC E

EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;

HOMO SAPIENS (HUMAN)

ACVRLK3

EUTHERIA; PRIMATES

SERINE/THREONINE-PROTEIN KINASE RECEPTOR R5 PRECURSOR (EC (SKR5) (ACTIVIN RECEPTOR-LIKE KINASE 3) (ALK-3).

01-JUN-1994 (REL. 29, CREATED) 01-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE) 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)

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STANDARD;

LI 3 KIRS HUMAN P36894;

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ò

2.7.1.37)

ö 240 480 120 180 240 420 480 DSGMPVVTSGCLGLEGSDFQCRDTPIPHQRRSIECCTERNECNKDLHPTLPPLKDRDFVD 120 gnihhkallisvtvcsillvliiifcyfrykrgearprysiglegdetyippgeslkdli 180 wfreteiyqtvlmrhenilgfiaadikgtgswtqlvlitdyhengslydylksttldtkg 300 mlklayssvsglchlhtgifstqgkpaiahrdlksknilvkkngtcciadlglavkfisd 360 tnevdippntrvgtkrymppevldeslnrnhfgsyimadmysfglilweiarrcvsggiv 420 Gaps dsgghlvtkgclglegsdfqcrdtpiphqrrsiecctgqdycnkhlnptlpplknrdfae 1 mpllsssklsmesrkedsegtapappqkklscqchhhcpedsvnstcstdgycftiieed eqsqssgsgsglpllvqrtiakqiqmvkqigkgrygevwmgkwrgekvavkvfftteeas ECSQSSGSGLPLLVQRTIAKQIQWVKQIGKGRYGFVWMGKWRGEKVAVKVFFTTEBAS TNEVDIPPNTRVGTKRYMPPEVLDESLNRNHFQSYIMADMYSFGLILWEIARRCVSGGIV GPIHHRALLISVIVCSLLIVLIIFFCYFRYKRQEARPRYSIGLEQDETYIPPGESLRDLI eeyqlpyhdlvpsdpsyedmreivcikrlrpsfpnrwssdeclrqmgklmmecwahnpas . 0 Length 502; Indels 23; Mismatches 19; Score 3466; DB 5; Pred. No. 0.00e+00; 502 502 rltalrvkktlakmsesqdikl 92.7%; 91.6%; 460; Conservative Best Local Similarity Query Match 241 Matches 19 121 181 241 361 481 61 301 361 421 481 121 181 301 421 g g ò ò 임 ò g Š 원 ò 임 à 엄 ò 엄 ద

ŝ Gaps ŝ Length 532 Query Match 73.7%; Score 2757; DB 5; Length 53 Best Local Similarity 71.9%; Pred. No. 0.00e+00; Matches 363; Conservative 76; Mismatches 61; Indels Distribution rights by Intelligenetics, Inc. ONCOGENE 8:2879-2887(1993).

XXXXX

protein - protein database search, using Smith-Waterman algorithm MPsrch pp

353.311 Million cell updates/sec MasPar time 4.68 Seconds Thu May 22 14:34:54 1997; Run on:

Tabular output not generated

1 MLLRSSGKLNVGTKKEDGES.....TALRVKKTLAKMSESQDIKL 502 (1-502) from US08436265.pep 3740 >US-08-436-265-18 Description: Perfect Score: Sequence:

o;

9 9 120 180

PAM 150 Gap Scoring table:

35845 segs, 3290575 residues Searched:

summaries Listing first 45 Minimum Match 0% -processing:

1:51 2:52 3:53 4:54 5:55 6:PCT90 7:PCT91 8:PCT52 9:PCT93 10:PCT94 11:PCT95 12:PCT96 a-1.5561 Database:

scale 0.206 . . Mean 33.828; Variance 163.878; Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| | Pred. No. | 0.00e+00 | 0.00e+00 | 1.10e-229 | 1.34e-229 | 1.05e-148 | 1.05e-148 | 9.82e-148 | 2.66e-135 | 2.48e-134 | 1.54e-133 | |
|------------|----------------------------------|---------------------------------|------------|------------|------------|------------|------------------------|------------------------|---------------|------------------------|------------------------|--------------------|
| | | Sequence 8, Applicatio 0.00e+00 | Applicatio | Applicatio | Applicatio | Applicati | Sequence 17, Applicati | Sequence 10, Applicati | 8, Applicatio | Sequence 4, Applicatio | Sequence 15, Applicati | |
| | uo | 80 | 4, | 9 | 2 | 17, | 17, | 10, | 80 | 4, | 15, | |
| | Description | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence 8 | Sequence | Sequence | |
| | ID | PCT-US95-0 | PCT-US94-1 | | PCT-US94-1 | US-08-317- | | PCT-US94-1 | PCT-US94-1 | PCT-US95-0 | US-08-149- | AT. T. C. NAMENITO |
| | DB | 11 | 10 | 11 | 10 | Ŋ | Ŋ | 10 | 10 | 11 | ß | |
| | Length | 502 11 | 502 | 532 | 532 | 501 | 501 | 503 | 505 | 509 | 501 | |
| \ 0 | ⊋Query Score ≟Match Length DB | 3740-100.0 | . 99.2 | 73.7 | 73.7 | 49.3 | 49.3 | 49.0 | 45.2 | 44.9 | 44.7 | |
| | Score | 3740 | 3711 | 2757 | 2756 | 1842 | 1842 | 1831 | 1690 | 1679 | 1670 | |
| | Kesult No. | - H | 73 | (1) | 4 | 5 | 9 | 7 | 8 | 6 | 07 | |

Ä. 502 PRT; STANDARD; PCT-US95-05467-8 01-JAN-1900 XXXXXX CSCSSEXEXEX

RESULT

Sequence 8, Application PC/TUS9505467
GENERAL INFORMATION:
APPLICANT:
APPLICANT:
TITLE OF INVENTION: MORPHOGENIC PR
TITLE OF INVENTION: SURFACE RECEPT

PC/TUS9505467

Sequence 8, Application

MORPHOGENIC PROTEIN-SPECIFIC CELL SURFACE RECEPTORS AND USES THEREFOR Ä 502 PRT; STANDARD; PCT-US94-10080-4 RESULT A X

241 WFRETEIYQTVLMRHENILGFIAADIKGTGSWTQLYLITDYHENGSLYDYLKSTTLDAKS 300 361 INEVDIPPNIRVGTKRYMPPEVLDESLNRNHFQSYIMADMYSFGLILWEIARRCVSGGIV 420 61 DSGTPVVTSGCLGLEGSDFQCRDTPIPHQRRSIECCTERNECNKDLHPTLPPLKDRDFVD 120 WFRETELYQTVLMRHENILGFIAADIKGTG.3VTQLYLITDYHENGSLYDYLKSTTLDAKS 300 MLKLAYSSVSGLCHLHTEIFSTQGKPAIAHRDLKSKNILVKKNGTCCIADLGLAVKFISD 360 TNEVDIPPNTRVGTKRYMPPEVLDESLNRTHFQSYIMADMYSFGLILWEIARRCVSGGIV 420 EEYQLPYHDLVPSDPSYEDMREIVCMKKLRPSFPNRWSSDECLRQMGKLMTECWAHNPAS 480 Gaps 61 DSGMPVVTSGCLGLEGSDFQCRDTPIPHQRRSIECCTERNECNKDLHPTLPPLKDRDFVD 1 MLLRSSGKINVGTKKEDGESTAPTPRPKILRCKCHHHCPEDSVNNICSTDGYCFTMIEED GPIHHKALLISVTVCSLLLVLIILFCYFRYKRQEARPRYSIGLEQDETYIPPGESLRDLI 301 MLKLAYSSVSGLCHLHTEIFSTQGKPAIAHRDLKSKNIIVKKNGTCCIADLGLAVKFISD 1 MLLASSGALMVGTKKEDGESTAPTARPKVLRCKCHHHCPEDSVNNICSTDGYCFTMIEED EQSQSSGSGSGLPLLVQRTIAKQIQMVKQIGKGRYGEVWMGKWRGEKVAVKVFFTTEEAS . 0 Length 502; 2; Indels Query Match 99.2%; Score 3711; DB 10; Best Local Similarity 99.0%; Pred. No. 0.00e+00; 3; Mismatches TITLE OF INVENTION: RECEPTOR PROTEINS APPLICANT: GENETICS INSTITUTE, INC Sequence 4, Application PC/TUS9410080 GENERAL INFORMATION: Sequence 4, Application PC/TUS9410080 RLTALRVKKTLAKMSESQDIKL 502 497; Conservative NUMBER OF SEQUENCES: 01-JAN-1900 Matches 121 (241 181 301 361 421 481 421 481 ద g 셤 CC CC 임 ò a 유 엄 유 à ò ð ò à ò ò ò

240 240 360